```
CC   produce 2 different mRNAs, one encoding a long form (bcl-XL), the
CC   other a short form (bcl-XS), lacking a stretch of 63 amino acids,
CC   by differential splicing of the 2nd coding exon to a more proximal
CC   5'-splice donor within the 1st coding exon.  Bcl-XS acts as a
CC   dominant negative regulator to bcl-XL activity, so it is preferable
CC   to use the bcl-XL cDNA for expression.  The gene may be modified to
CC   facilitate interaction with costimulatory Bax protein and inhibit
CC   interaction with antagonistic Bad protein, by modification of the
CC   Bcl-2 homology domains BH1 and/or BH2.  The bcl-XL gene may be
CC   introduced into T-cells in vivo or ex vivo via gene transfer using
CC   a vector for HIV infection gene therapy, to augment intracellular
CC   bcl-XL protein levels and protect from cell death.  A corresponding
CC   antisense oligonucleotide or expression vector may be used in gene
CC   therapy of e.g. autoimmune disease, graft rejection or graft-
CC   versus-host disease, to induce cell death (e.g. apoptosis) and
CC   down-regulate the immune response in a T-lymphocyte population.
SQ   Sequence   926 BP;    220 A;    249 C;    264 G;    193 T;

  Query Match             22.5%;  Score 131;  DB 1;  Length 926;
  Best Local Similarity   56.3%;  Pred. No. 8.7e-24;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy      98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
           || ||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db     364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy     158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
           | ||    || | ||||||  | |||  ||| ||| |  | |||||  ||  | |||||||
Db     424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy     218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggcccccaact 277
           |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db     484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy     278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
           |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db     544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy     338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
           |||||||| |   | ||||| | |   |    |  |||||||   | ||||||  |    |
Db     604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy     398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
             || |     ||||||||     |  || |||||||     ||     |  || || |||
Db     664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy     458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
           ||   ||    | |||   ||        | |||  |   |       |   |   ||| |
Db     724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

Qy     518 tgctgacgggggccg 532
              |||| | |||||
Db     784 GCATGACTGTGGCCG 798


RESULT  15
X33182
ID   X33182 standard; DNA; 7372 BP.
AC   X33182;
DT   25-JUN-1999  (first entry)
DE   Base sequence of the plasmid pRx-Bcl-xl-bsr.
KW   Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
KW   crmA; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer;
KW   autoimmune disease; graft rejection reaction; inflammation;
KW   inflammatory disease; ss.
OS   Synthetic.
OS   Homo sapiens.
PN   WO9913073-A2.
PD   18-MAR-1999.
PF   07-SEP-1998; J04010.
PR   08-SEP-1997; JP-259235.
PA   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
PI   Hamada H;
DR   WPI; 99-243728/20.
PT   New apoptosis-resistant virus-sensitive cell
PS   Example 2; Page 41-45; 51pp; English.
CC   The present invention describes an apoptosis-resistant virus-sensitive
CC   cell line into which an apoptosis resistance gene has been introduced.
CC   The recombinant viruses generated are capable of expressing apoptosis-
CC   associated genes. These can then be used in a variety of diseases for
CC   which the induction of apoptosis by gene transfer, or where the
CC   inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC   are useful as vectors for gene therapy which can be applied to cancer
CC   therapy for destroying cancer cells selectively, the treatment of
CC   autoimmune diseases and graft rejection reaction, and apoptosis induction
CC   therapy for inflammatory cells in inflammatory diseases. Prior arts have
CC   encountered the problem where if an adenovirus vector capable of
CC   expressing an apoptosis-associated gene is introduced into animal cells,
CC   the cells producing the virus will be destroyed because the period of
CC   time required to induce cell death by apoptosis is shorter than that
CC   required to replicate and produce the virus, resulting in failure to
CC   obtain a recombinant virus having the integrated apoptosis-associated
CC   gene. In this invention an apoptosis-resistant 293 cell line (having an
CC   apoptosis resistant gene introduced) is established and overcomes the
CC   problem. The present sequence represents the base sequence of the
CC   plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and
CC   is used in an example from the present invention.
SQ   Sequence   7372 BP;    2353 A;    1749 C;    1649 G;    1621 T;

  Query Match             22.5%;  Score 131;  DB 1;  Length 7372;
  Best Local Similarity   56.3%;  Pred. No. 1.3e-23;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy      98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
           || ||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db    2302 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 2361

Qy     158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
           | ||    || | ||||||  | |||  ||| ||| |  | |||||  ||  | |||||||
Db    2362 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 2421

Qy     218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggcccccaact 277
           |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db    2422 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 2481

Qy     278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
           |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db    2482 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 2541

Qy     338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
           |||||||| |   | ||||| | |   |    |  |||||||   | |||||| |    |
Db    2542 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 2601

Qy     398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
             || |     ||||||||     |  || |||||||     ||     |  || || |||
Db    2602 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 2661

Qy     458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
           ||   ||    | |||   ||        | |||  |   |       |   |   ||| |
Db    2662 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 2721

Qy     518 tgctgacgggggccg 532
              |||| | |||||
Db    2722 GCATGACTGTGGCCG 2736


Search completed: July  4, 2000, 01:26:24
Job time: 14671 sec
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CC   which tissues they are most highly expressed in (see V59511 for described
CC   uses).
SQ   Sequence   1864 BP;    494 A;    403 C;    506 G;    455 T;

  Query Match            72.7%;  Score 423.6;  DB 1;  Length 1864;
  Best Local Similarity  98.6%;  Pred. No. 8.3e-96;
  Matches  426;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db    131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db    371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy    421 agtgggggctgg 432
          ||||||||||||
Db    431 AGTGGGGGCTGG 442


RESULT  13
Q81698
ID   Q81698 standard; DNA; 926 BP.
AC   Q81698;
DT   10-AUG-1995  (first entry)
DE   Human thymus BCL-XL DNA.
KW   BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;
KW   autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
KW   multiple sclerosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             135. .836
FT                   /*tag= a
PN   WO9500642-A.
PD   05-JAN-1995.
PF   22-JUN-1994; U07089.
PR   22-JUN-1993; US-081448.
PA   (ARCH-) ARCH DEV CORP.
PA   (UNMI ) UNIV MICHIGAN.
PI   Boise LH,  Nunez G,  Thompson CB;
DR   WPI; 95-052079/07.
DR   P-PSDB; R68887.
PT   New poly-nucleotide encoding new poly-peptide(s) that modify
PT   apoptosis - and related vectors, recombinant cells and
PT   antibodies, useful in assay and for control of cell death in e.g.
PT   neuronal cells, lymphocytes and cancers
PS   Claim 5; Page 94; 127pp; English.
CC   This DNA may be expressed recombinantly for the production of a BCL-
CC   X protein, particularly with pcmV plasmids as vectors for
CC   expression in mammalian cell cultures.  The protein has particular
CC   application in cancer cells (failure of programed cell death (PCD))
CC   or neurodegenerative and autoimmune diseases (premature PCD), e.g.
CC   Parkinson's disease, amylotrophic lateral sclerosis and multiple
CC   sclerosis.
SQ   Sequence   926 BP;    220 A;    249 C;    264 G;    193 T;

  Query Match            22.5%;  Score 131;  DB 1;  Length 926;
  Best Local Similarity  56.3%;  Pred. No. 8.7e-24;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy     98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
          || |||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db    364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy    158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
          | ||    || | |||||||  | |||  ||| ||| |  | |||||  ||  | |||||||
Db    424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy    218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaact 277
          |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db    484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy    278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
          |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db    544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy    338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
          |||||||| |   | ||||| | |   |     |  |||||||   | ||||||  |    |
Db    604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy    398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
            || |     ||||||||    |  || |||||||     ||     |  || || |||
Db    664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy    458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
          ||  ||    | |||   ||     | |||  |   |     |   |   ||| |
Db    724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

Qy    518 tgctgacgggggccg 532
            |||| | |||||
Db    784 GCATGACTGTGGCCG 798


RESULT  14
T40079
ID   T40079 standard; cDNA; 926 BP.
AC   T40079;
DT   30-MAR-1997  (first entry)
DE   Bcl-XL gene.
KW   Human; bcl-XL; T-lymphocyte; cell death; gene therapy; HIV; AIDS;
KW   antisense; immune disorder; autoimmune disease; graft rejection;
KW   graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             135. .836
FT                   /*tag= a
FT                   /product= Human bcl-XL protein
PN   WO9634956-A1.
PD   07-NOV-1996.
PF   02-MAY-1996; U06203.
PR   04-MAY-1995; US-435518.
PR   07-JUN-1995; US-481739.
PA   (ARCH-) ARCH DEV CORP.
PA   (USNA ) US SEC OF NAVY.
PI   June CH,  Thompson CB;
DR   WPI; 96-506159/50.
DR   P-PSDB; W05821.
PT   Inducing or preventing death of T cells by bcl-XL protein regulation
PT   - used to increase survival of HIV infected cells or to
PT   down:regulate immune responses in immune diseases
PS   Disclosure; Page 51-52; 76pp; English.
CC   This sequence encodes human bcl-XL protein, which protects
CC   T-lymphocytes against cell death.  The genomic bcl-X gene may
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Qy    421 agtgggggctgg 432
          ||||||||||||
Db    421 AGTGGGGGCTGG 432
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RESULT 12
V59630
ID V59630 standard; DNA; 1864 BP.
AC V59630;
DT 19-JAN-1999 (first entry)
DE Human secreted protein gene 120 clone HGBGZ64.
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9839448-A2.
PD 11-SEP-1998.
PF 06-MAR-1998; U04493.
PR 02-OCT-1997; US-061060.
PR 07-MAR-1997; US-038621.
PR 07-MAR-1997; US-040161.
PR 07-MAR-1997; US-040162.
PR 07-MAR-1997; US-040163.
PR 07-MAR-1997; US-040333.
PR 07-MAR-1997; US-040334.
PR 07-MAR-1997; US-040336.
PR 07-MAR-1997; US-040626.
PR 11-APR-1997; US-043311.
PR 11-APR-1997; US-043312.
PR 11-APR-1997; US-043313.
PR 11-APR-1997; US-043314.
PR 11-APR-1997; US-043568.
PR 11-APR-1997; US-043569.
PR 11-APR-1997; US-043576.
PR 11-APR-1997; US-043578.
PR 11-APR-1997; US-043580.
PR 11-APR-1997; US-043669.
PR 11-APR-1997; US-043670.
PR 11-APR-1997; US-043671.
PR 11-APR-1997; US-043672.
PR 11-APR-1997; US-043674.
PR 23-MAY-1997; US-047492.
PR 23-MAY-1997; US-047500.
PR 23-MAY-1997; US-047501.
PR 23-MAY-1997; US-047502.
PR 23-MAY-1997; US-047503.
PR 23-MAY-1997; US-047581.
PR 23-MAY-1997; US-047582.
PR 23-MAY-1997; US-047583.
PR 23-MAY-1997; US-047584.
PR 23-MAY-1997; US-047585.
PR 23-MAY-1997; US-047586.
PR 23-MAY-1997; US-047587.
PR 23-MAY-1997; US-047588.
PR 23-MAY-1997; US-047589.
PR 23-MAY-1997; US-047590.
PR 23-MAY-1997; US-047592.
PR 23-MAY-1997; US-047593.
PR 23-MAY-1997; US-047594.
PR 23-MAY-1997; US-047595.
PR 23-MAY-1997; US-047596.
PR 23-MAY-1997; US-047597.
PR 23-MAY-1997; US-047598.
PR 23-MAY-1997; US-047599.
PR 23-MAY-1997; US-047600.
PR 23-MAY-1997; US-047601.
PR 23-MAY-1997; US-047612.
PR 23-MAY-1997; US-047613.
PR 23-MAY-1997; US-047614.
PR 23-MAY-1997; US-047615.
PR 23-MAY-1997; US-047617.
PR 23-MAY-1997; US-047618.
PR 23-MAY-1997; US-047632.
PR 23-MAY-1997; US-047633.
PR 06-JUN-1997; US-048964.
PR 06-JUN-1997; US-048974.
PR 13-JUN-1997; US-049610.
PR 08-JUL-1997; US-051926.
PR 16-JUL-1997; US-052874.
PR 18-AUG-1997; US-055724.
PR 22-AUG-1997; US-056630.
PR 22-AUG-1997; US-056631.
PR 22-AUG-1997; US-056632.
PR 22-AUG-1997; US-056636.
PR 22-AUG-1997; US-056637.
PR 22-AUG-1997; US-056662.
PR 22-AUG-1997; US-056664.
PR 22-AUG-1997; US-056845.
PR 22-AUG-1997; US-056862.
PR 22-AUG-1997; US-056864.
PR 22-AUG-1997; US-056872.
PR 22-AUG-1997; US-056874.
PR 22-AUG-1997; US-056875.
PR 22-AUG-1997; US-056876.
PR 22-AUG-1997; US-056877.
PR 22-AUG-1997; US-056878.
PR 22-AUG-1997; US-056879.
PR 22-AUG-1997; US-056880.
PR 22-AUG-1997; US-056881.
PR 22-AUG-1997; US-056882.
PR 22-AUG-1997; US-056884.
PR 22-AUG-1997; US-056886.
PR 22-AUG-1997; US-056887.
PR 22-AUG-1997; US-056888.
PR 22-AUG-1997; US-056889.
PR 22-AUG-1997; US-056892.
PR 22-AUG-1997; US-056893.
PR 22-AUG-1997; US-056894.
PR 22-AUG-1997; US-056903.
PR 22-AUG-1997; US-056908.
PR 22-AUG-1997; US-056909.
PR 22-AUG-1997; US-056910.
PR 22-AUG-1997; US-056911.
PR 05-SEP-1997; US-057650.
PR 05-SEP-1997; US-057669.
PR 05-SEP-1997; US-057761.
PR 12-SEP-1997; US-058785.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
DR WPI; 98-506364/43.
DR P-PSDB; W74848.
PT New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 353-354; 721pp; English.
CC This sequence represents a nucleic acid molecule designated Gene 120 from
CC the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and ATCC
CC 209048) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. V59502) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on

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PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   P-PSDB; Y05533.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Disclosure; Page 38; 52pp; English.
CC   The present sequence is described as a derivative of the mouse
CC   bcl-w gene (see X25133) and encodes Bcl-w protein (see Y05533), a
CC   pro-survival member of the Bcl-2 family which is widely expressed
CC   and which is essential for spermatogenesis.  The invention relates
CC   generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for
CC   inducing or reducing fertility of male animals.  Methods are
CC   provided for the treatment of infertility, or for reducing
CC   fertility, by modulating spermatogenesis.  An animal model carries
CC   a mutation is at least one allele of the human or murine bcl-w gene
CC   or in a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   581 BP;    105 A;    164 C;    195 G;    117 T;
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  Query Match             85.9%;  Score 501;  DB 1;  Length 581;
  Best Local Similarity   91.4%;  Pred. No. 5.5e-115;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||| ||||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db      1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          | |||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||||| || ||||  ||||||||||||||||
Db    361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||| |||||||||| |||||||||||||||||||||||||||||||||||||||| ||| |||
Db    421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581
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RESULT  11
V41925
ID   V41925 standard; cDNA; 1098 BP.
AC   V41925;
DT   20-NOV-1998  (first entry)
DE   Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .1098
FT                   /*tag= a
FT                   /product= "Bcl-like (HAICH29) protein"
PN   WO9831800-A2.
PD   23-JUL-1998.
PF   21-JAN-1998; U00960.
PR   21-JAN-1997; US-034205.
PR   21-JAN-1997; US-034204.
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
PI   Su JY;
DR   WPI; 98-414099/35.
DR   P-PSDB; W59884.
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
PS   Claim 2; Fig 12A-12D; 120pp; English.
CC   This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
SQ   Sequence   1098 BP;    264 A;    279 C;    325 G;    230 T;
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  Query Match             72.7%;  Score 424;  DB 1;  Length 1098;
  Best Local Similarity   98.8%;  Pred. No. 5.9e-96;
  Matches  427;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttcttt 300
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420
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SQ   Sequence   581 BP;    106 A;    158 C;    200 G;    117 T;

  Query Match            89.5%;  Score 521.8;  DB 1;  Length 581;
  Best Local Similarity  93.6%;  Pred. No. 4.2e-120;
  Matches  544;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          |||||||||||||||  |||||||||||||||||| ||||| ||||||||||| |||
Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          |||||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
           |||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||| |||||||||||||||||||||| || ||||  ||||||||||||||||
Db    361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   9
T96578
ID   T96578 standard; DNA; 581 BP.
AC   T96578;
DT   22-APR-1998  (first entry)
DE   Mouse bcl-w DNA.
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .507
FT                   /*tag= a
FT                   /product= bcl-w
FT                   /note= "q"
PN   WO9735971-A1.
PD   02-OCT-1997.
PF   27-MAR-1997; AU0199.
PR   27-MAR-1996; AU-008965.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR   WPI; 97-489635/45.
DR   P-PSDB; W36048.
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
PS   Claim 3; Page 50-51; 86pp; English.
CC   This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
CC   family. This gene promotes cell survival, so its modulation is useful in
CC   treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
CC   stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
CC   hypoxia, ischaemia, human immunodeficiency virus infection or in cell
CC   transplants. Up-regulation of the gene can also be used to modify cell
CC   lines cultured in vivo, e.g. to develop new lines, to facilitate
CC   isolation of hybridomas and to increase survival of primary explants
CC   during genetic modification. It can be used to produce recombinant Bcl-w
CC   for therapy, diagnosis, antibody production or screening of potential
CC   modulators.
SQ   Sequence   581 BP;    105 A;    164 C;    195 G;    117 T;

  Query Match            85.9%;  Score 501;  DB 1;  Length 581;
  Best Local Similarity  91.4%;  Pred. No. 5.5e-115;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||| |||
Db      1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          | |||||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
           |||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||| ||||| ||||| |||||||||||||||| || ||||  ||||||||||||||||
Db    361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||| |||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT  10
X25135
ID   X25135 standard; DNA; 581 BP.
AC   X25135;
DT   05-JUL-1999  (first entry)
DE   Mouse bcl-w gene derivative.
KW   Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW   animal model; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .507
FT                   /*tag= a
PN   WO9913710-A1.
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Db    361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
          |||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 7
X15945
ID X15945 standard; cDNA; 579 BP.
AC X15945;
DT 20-MAY-1999 (first entry)
DE cDNA encoding the rat bcl-y protein.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.
OS Rattus sp.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
DR P-PSDB; W97391.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 13-16; 26pp; English.
CC The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;

Query Match 89.7%; Score 523; DB 1; Length 579;
Best Local Similarity 94.0%; Pred. No. 2.1e-120;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Db     61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||||||||||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          |||||||||||| |||||||||||||||||||||||| || ||||| ||| ||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||| |||||||| |||||||||||| ||  |||  ||||||||||||||||
Db    361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
          |||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
```

RESULT 8
X25133
ID X25133 standard; DNA; 581 BP.
AC X25133;
DT 05-JUL-1999 (first entry)
DE Mouse bcl-w gene.
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW animal model; ss.
OS Mus sp.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR P-PSDB; Y05531.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Claim 3; Page 34; 52pp; English.
CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein
CC (see Y05531), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation is at least one allele of the human or
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
CC have disorganised seminferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of
CC inducing, enhancing or otherwise facilitating spermatogenesis in
CC animals, or which can induce infertility.

OS Homo sapiens.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
DR P-PSDB; W97392.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 15-16; 26pp; English.
CC The present sequence encodes human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;

Query Match 97.4%; Score 567.8; DB 1; Length 579;
Best Local Similarity 98.8%; Pred. No. 1.9e-131;
Matches 572; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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Db    121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
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Db    241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 6
V28333
ID V28333 standard; cDNA; 579 BP.
AC V28333;
DT 02-OCT-1998 (first entry)
DE Rat bcl-y gene.
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 1. .579
FT /*tag= a
FT /product= bcl-y
FT /note= "No stop codon given"
PN US5789201-A.
PD 04-AUG-1998.
PF 11-FEB-1997; 798897.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 98-446079/38.
DR P-PSDB; W61391.
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
PS Claim 2; Column 13/14; 27pp; English.
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontrolled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;

Query Match 89.7%; Score 523; DB 1; Length 579;
Best Local Similarity 94.0%; Pred. No. 2.1e-120;
Matches 544; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
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Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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CC   inducing, enhancing or otherwise facilitating spermatogenesis in
CC   animals, or which can induce infertility.
SQ   Sequence   581 BP;    104 A;    155 C;    210 G;    112 T;


  Query Match            98.3%;  Score 573;  DB 1;  Length 581;
  Best Local Similarity  99.1%;  Pred. No. 1e-132;
  Matches  576;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttctttt 300
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Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   4
V28334
ID   V28334 standard; cDNA; 579 BP.
AC   V28334;
DT   02-OCT-1998  (first entry)
DE   Human bcl-y gene.
KW   ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .579
FT                   /*tag=  a
FT                   /product= bcl-y
FT                   /note= "No stop codon given"
PN   US5789201-A.
PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   P-PSDB; W61392.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Claim 3; Column 15/16; 27pp; English.
CC   The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC   family, components in the cell death pathway.  The bcl-2 family
CC   have both apoptotic activity and the apoptosis blocking activity.  bcl-y
CC   falls in the apoptosis activity category.  The  recombinant protein may
CC   be used to prevent uncontrolled cell growth, either by its direct
CC   administration to recombinant genetic constructs to increase its
CC   expression in vivo.  Also, antisense constructs can be used in disorders
CC   where prevention of cell death is desired.
SQ   Sequence   579 BP;    106 A;    154 C;    208 G;    111 T;


  Query Match            97.4%;  Score 567.8;  DB 1;  Length 579;
  Best Local Similarity  98.8%;  Pred. No. 1.9e-131;
  Matches  572;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Db    121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttctttt 300
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

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RESULT   5
X15946
ID   X15946 standard; cDNA; 579 BP.
AC   X15946;
DT   20-MAY-1999  (first entry)
DE   cDNA encoding the human bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite; ss.
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Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
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Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtgaa 583
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
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RESULT 2
X25134
ID X25134 standard; DNA; 583 BP.
AC X25134;
DT 05-JUL-1999 (first entry)
DE Human bcl-w gene derivative.
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR P-PSDB; Y05532.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 36; 52pp; English.
CC The present sequence is described as a derivative of the human
CC bcl-w gene (see X25132) and encodes Bcl-w protein (see Y05532), a
CC pro-survival member of the Bcl-2 family which is widely expressed
CC and which is essential for spermatogenesis. The invention relates
CC generally to a method of treatment and to an animal model for the
CC identification of molecules and genetic sequences useful for
CC inducing or reducing fertility of male animals. Methods are
CC provided for the treatment of infertility, or for reducing
CC fertility, by modulating spermatogenesis. An animal model carries
CC a mutation is at least one allele of the human or murine bcl-w gene
CC or in a gene associated with bcl-w. Such animals have disorganised
CC seminferous tubules and are substantially infertile, but possess no
CC other major abnormalities as determined by histological examination.
CC They can be used to screen for therapeutic molecules including
CC genetic sequences capable of inducing, enhancing or otherwise
CC facilitating spermatogenesis in animals, or which can induce
CC infertility.
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

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  Query Match             100.0%;  Score 583;  DB 1;  Length 583;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-135;
  Matches  583;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Qy    481 cgtctgcgggagggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtgaa 583
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 583
```

RESULT 3
X25132
ID X25132 standard; DNA; 581 BP.
AC X25132;
DT 05-JUL-1999 (first entry)
DE Human bcl-w gene.
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR P-PSDB; Y05530.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Claim 3; Page 32; 52pp; English.
CC The present sequence is the human bcl-w gene encoding Bcl-w protein
CC (see Y05530), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation is at least one allele of the human or
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
CC have disorganised seminferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 21:21:53 ; Search time 115.05 Seconds
(without alignments)
1267.814 Million cell updates/sec

Title: US-09-155-327B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	583	100.0	583	1	T96577	Human bcl-w DNA. N
	2	583	100.0	583	1	X25134	Human bcl-w gene d
	3	573	98.3	581	1	X25132	Human bcl-w gene.
	4	567.8	97.4	579	1	V28334	Human bcl-y gene.
	5	567.8	97.4	579	1	X15946	cDNA encoding the
	6	523	89.7	579	1	V28333	Rat bcl-y gene. Nu
	7	523	89.7	579	1	X15945	cDNA encoding the
	8	521.8	89.5	581	1	X25133	Mouse bcl-w gene.
	9	501	85.9	581	1	T96578	Mouse bcl-w DNA. N
	10	501	85.9	581	1	X25135	Mouse bcl-w gene d
	11	424	72.7	1098	1	V41925	Nucleotide sequenc
	12	423.6	72.7	1864	1	V59630	Human secreted pro
	13	131	22.5	926	1	Q81698	Human thymus BCL-X
	14	131	22.5	926	1	T40079	Bcl-XL gene. Induc
	15	131	22.5	7372	1	X33182	Base sequence of t
	16	123.4	21.2	765	1	Q49815	Bcl-2. Treating tu
	17	123.4	21.2	953	1	X33183	Bcl-2 DNA fragment
	18	123.4	21.2	5086	1	Q54631	Human oncogene bcl
	19	123.4	21.2	5086	1	Q86661	Human bcl-2 gene.
	20	123.4	21.2	5105	1	N81292	Sequence of bcl-2
	21	123.4	21.2	7996	1	X33184	Base sequence of t
	22	121.8	20.9	760	1	T33694	Human BCL2 cDNA. S
	23	120.4	20.7	1384	1	V17638	Mouse BCL-x gamma
	24	119	20.4	615	1	Q73987	Human bcl-2 gene O
	25	119	20.4	911	1	X08431	bcl-2 proto-oncoge
	26	115.8	19.9	831	1	N81293	Sequence of bcl-2
	27	113.8	19.5	1274	1	Q81696	Chicken lymphoid B
	28	52.6	9.0	737	1	Q81699	Human thymus BCL-X
	29	52.2	9.0	822	1	T48488	Bax omega protein
	30	51.8	8.9	624	1	Q97606	Human Bax protein
	31	51.8	8.9	624	1	V84005	cDNA encoding a hu
c	32	45.6	7.8	509	1	V89057	EST clone CB239. N
	33	44.4	7.6	5408	1	Q95494	Human Cdn-3 DNA. N
	34	44	7.5	114955	1	X53491	Human adenosine A1
	35	40	6.9	3690	1	Q30849	Type III procollag
	36	40	6.9	5460	1	T16508	Vector pAC3A1 cont
c	37	38	6.5	3004	1	V62162	HSV-2 strain SB5 C
c	38	38	6.5	117213	1	V62176	HSV-2 strain SB5 C
	39	37.8	6.5	1505	1	Q55750	Genomic clone G11F
	40	37.8	6.5	3293	1	T05810	Human thyroid tran
	41	37.2	6.4	4289	1	V62147	HSV-2 strain SB5 C
	42	37	6.3	6843	1	T84509	Human LDL receptor
	43	37	6.3	14928	1	Q11707	Immunoglobulin D-r
	44	36	6.2	1286	1	T42139	Bak-2 gene. Screen
	45	36	6.2	6511	1	Q95493	Human Cdn-2 DNA. N

ALIGNMENTS

RESULT 1
T96577
ID T96577 standard; DNA; 583 BP.
AC T96577;
DT 22-APR-1998 (first entry)
DE Human bcl-w DNA.
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1. .582
FT /*tag= a
FT /product= bcl-w
PN WO9735971-A1.
PD 02-OCT-1997.
PF 27-MAR-1997; AU0199.
PR 27-MAR-1996; AU-008965.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR WPI; 97-489635/45.
DR P-PSDB; W36047.
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
PS Claim 3; Page 48; 86pp; English.
CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC family, extracted from an adult brain library. This gene promotes cell
CC survival, so its modulation is useful in treatment of cancer or
CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
CC human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T;

Query Match 100.0%; Score 583; DB 1; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CC dominant negative regulator to bcl-XL activity, so it is preferable
CC to use the bcl-XL cDNA for expression. The gene may be modified to
CC facilitate interaction with costimulatory Bax protein and inhibit
CC interaction with antagonistic Bad protein, by modification of the
CC Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be
CC introduced into T-cells in vivo or ex vivo via gene transfer using
CC a vector for HIV infection gene therapy, to augment intracellular
CC bcl-XL protein levels and protect from cell death. A corresponding
CC antisense oligonucleotide or expression vector may be used in gene
CC therapy of e.g. autoimmune disease, graft rejection or graft-
CC versus-host disease, to induce cell death (e.g. apoptosis) and
CC down-regulate the immune response in a T-lymphocyte population.
SQ Sequence 926 BP; 220 A; 249 C; 264 G; 193 T;

Query Match 23.2%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

```
Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          |||||  |  | |||||  ||| | ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | |||||  ||||  |  ||    ||||||||  ||  |||||||  || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || |||||  |  || || ||  |||| || ||| ||   |||||| | |   ||
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | |||||| |   | |||||| |    |  || |     ||||||||    |  ||||
Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||   ||    |  ||    ||       |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
          |||  ||  |      ||  |   || |  |||| | |||||
Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
```

RESULT 15
X33182
ID X33182 standard; DNA; 7372 BP.
AC X33182;
DT 25-JUN-1999 (first entry)
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.
KW Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
KW crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
KW autoimmune disease; graft rejection reaction; inflammation;
KW inflammatory disease; ss.
OS Synthetic.
OS Homo sapiens.
PN WO9913073-A2.
PD 18-MAR-1999.
PF 07-SEP-1998; J04010.
PR 08-SEP-1997; JP-259235.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
PI Hamada H;
DR WPI; 99-243728/20.
PT New apoptosis-resistant virus-sensitive cell
PS Example 2; Page 41-45; 51pp; English.
CC The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.
CC The recombinant viruses generated are capable of expressing apoptosis-
CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene therapy which can be applied to cancer
CC therapy for destroying cancer cells selectively, the treatment of
CC autoimmune diseases and graft rejection reaction, and apoptosis induction
CC therapy for inflammatory cells in inflammatory diseases. Prior arts have
CC encountered the problem where if an adenovirus vector capable of
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC the cells producing the virus will be destroyed because the period of
CC time required to induce cell death by apoptosis is shorter than that
CC required to replicate and produce the virus, resulting in failure to
CC obtain a recombinant virus having the integrated apoptosis-associated
CC gene. In this invention an apoptosis-resistant 293 cell line (having an
CC apoptosis resistant gene introduced) is established and overcomes the
CC problem. The present sequence represents the base sequence of the
CC plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and
CC is used in an example from the present invention.
SQ Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T;

Query Match 23.2%; Score 134.6; DB 1; Length 7372;
Best Local Similarity 58.3%; Pred. No. 4.5e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

```
Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db   2332 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 2391

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          |||||  |  | |||||  ||| | ||||||||  ||||  | ||  ||||    |||||
Db   2392 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 2451

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | |||||  ||||  |  ||    ||||||||  ||  |||||||  || ||   ||| |
Db   2452 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 2511

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || |||||  |  || || ||  |||| || ||| ||   |||||| | |   ||
Db   2512 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 2571

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | |||||| |   | |||||| |    |  || |     ||||||||    |  ||||
Db   2572 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 2631

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||   ||    |  ||    ||       |
Db   2632 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 2691

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
          |||  ||  |      ||  |   || |  |||| | |||||
Db   2692 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 2736
```

Search completed: July 4, 2000, 01:26:28
Job time: 14675 sec

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CC   which tissues they are most highly expressed in (see V59511 for described
CC   uses).
SQ   Sequence   1864 BP;    494 A;    403 C;    506 G;    455 T;

  Query Match            62.7%;  Score 364.4;  DB 1;  Length 1864;
  Best Local Similarity  90.0%;  Pred. No. 7.6e-89;
  Matches  389;  Conservative    1;  Mismatches   42;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| |||||||||||||  |||||||||||||| ||||| ||||| ||||||||||| |||
Db     11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 130

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          |||||||||||||||||||||| ||:||||| ||||| |||||||| ||||| ||||||
Db    131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db    191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 250

Qy    241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
          ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db    251 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggga 360
          |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||||| || ||||||||||||||||||||
Db    371 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 430

Qy    421 agtggcggctgg 432
          ||||| ||||||
Db    431 AGTGGGGGCTGG 442


RESULT  13
Q81698
ID   Q81698 standard; DNA; 926 BP.
AC   Q81698;
DT   10-AUG-1995  (first entry)
DE   Human thymus BCL-XL DNA.
KW   BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;
KW   autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
KW   multiple sclerosis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             135. .836
FT                   /*tag=  a
PN   WO9500642-A.
PD   05-JAN-1995.
PF   22-JUN-1994; U07089.
PR   22-JUN-1993; US-081448.
PA   (ARCH-) ARCH DEV CORP.
PA   (UNMI ) UNIV MICHIGAN.
PI   Boise LH,  Nunez G,  Thompson CB;
DR   WPI; 95-052079/07.
DR   P-PSDB; R68887.
PT   New poly-nucleotide encoding new poly-peptide(s) that modify
PT   apoptosis - and related vectors, recombinant cells and
PT   antibodies, useful in assay and for control of cell death in e.g.
PT   neuronal cells, lymphocytes and cancers
PS   Claim 5; Page 94; 127pp; English.
CC   This DNA may be expressed recombinantly for the production of a BCL-
CC   X protein, particularly with pcmV plasmids as vectors for
CC   expression in mammalian cell cultures.  The protein has particular
CC   application in cancer cells (failure of programed cell death (PCD))
CC   or neurodegenerative and autoimmune diseases (premature PCD), e.g.
CC   Parkinson's disease, amylotrophic lateral sclerosis and multiple
CC   sclerosis.
SQ   Sequence   926 BP;    220 A;    249 C;    264 G;    193 T;

  Query Match            23.2%;  Score 134.6;  DB 1;  Length 926;
  Best Local Similarity  58.3%;  Pred. No. 2.6e-27;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          |||||  |  | |||||  ||| |  ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  ||||||| || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || ||||| |  || || ||  |||| || ||| ||   |||||| | |   ||
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | ||||||  |   | ||||||  |     |  ||  |      ||||||||    |  ||||
Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||      ||     |  || || ||| ||   ||     |  ||     ||      |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
            |||  ||  |      ||  |     || |  |||| | |||||
Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT  14
T40079
ID   T40079 standard; cDNA; 926 BP.
AC   T40079;
DT   30-MAR-1997  (first entry)
DE   Bcl-XL gene.
KW   Human; bcl-XL; T-lymphocyte; cell death; gene therapy; HIV; AIDS;
KW   antisense; immune disorder; autoimmune disease; graft rejection;
KW   graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             135. .836
FT                   /*tag=  a
FT                   /product= Human bcl-XL protein
PN   WO9634956-A1.
PD   07-NOV-1996.
PF   02-MAY-1996; U06203.
PR   04-MAY-1995; US-435518.
PR   07-JUN-1995; US-481739.
PA   (ARCH-) ARCH DEV CORP.
PA   (USNA ) US SEC OF NAVY.
PI   June CH,  Thompson CB;
DR   WPI; 96-506159/50.
DR   P-PSDB; W05821.
PT   Inducing or preventing death of T cells by bcl-XL protein regulation
PT   - used to increase survival of HIV infected cells or to
PT   down:regulate immune responses in immune diseases
PS   Disclosure; Page 51-52; 76pp; English.
CC   This sequence encodes human bcl-XL protein, which protects
CC   T-lymphocytes against cell death.  The genomic bcl-X gene may
CC   produce 2 different mRNAs, one encoding a long form (bcl-XL), the
CC   other a short form (bcl-XS), lacking a stretch of 63 amino acids,
CC   by differential splicing of the 2nd coding exon to a more proximal
CC   5'-splice donor within the 1st coding exon.  Bcl-XS acts as a
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```
Qy    421 agtggcggctgg 432
          ||||| ||||||
Db    421 AGTGGGGGCTGG 432
```

RESULT 12
V59630
ID V59630 standard; DNA; 1864 BP.
AC V59630;
DT 19-JAN-1999 (first entry)
DE Human secreted protein gene 120 clone HGBGZ64.
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
PN WO9839448-A2.
PD 11-SEP-1998.
PF 06-MAR-1998; U04493.
PR 02-OCT-1997; US-061060.
PR 07-MAR-1997; US-038621.
PR 07-MAR-1997; US-040161.
PR 07-MAR-1997; US-040162.
PR 07-MAR-1997; US-040163.
PR 07-MAR-1997; US-040333.
PR 07-MAR-1997; US-040334.
PR 07-MAR-1997; US-040336.
PR 07-MAR-1997; US-040626.
PR 11-APR-1997; US-043311.
PR 11-APR-1997; US-043312.
PR 11-APR-1997; US-043313.
PR 11-APR-1997; US-043314.
PR 11-APR-1997; US-043568.
PR 11-APR-1997; US-043569.
PR 11-APR-1997; US-043576.
PR 11-APR-1997; US-043578.
PR 11-APR-1997; US-043580.
PR 11-APR-1997; US-043669.
PR 11-APR-1997; US-043670.
PR 11-APR-1997; US-043671.
PR 11-APR-1997; US-043672.
PR 11-APR-1997; US-043674.
PR 23-MAY-1997; US-047492.
PR 23-MAY-1997; US-047500.
PR 23-MAY-1997; US-047501.
PR 23-MAY-1997; US-047502.
PR 23-MAY-1997; US-047503.
PR 23-MAY-1997; US-047581.
PR 23-MAY-1997; US-047582.
PR 23-MAY-1997; US-047583.
PR 23-MAY-1997; US-047584.
PR 23-MAY-1997; US-047585.
PR 23-MAY-1997; US-047586.
PR 23-MAY-1997; US-047587.
PR 23-MAY-1997; US-047588.
PR 23-MAY-1997; US-047589.
PR 23-MAY-1997; US-047590.
PR 23-MAY-1997; US-047592.
PR 23-MAY-1997; US-047593.
PR 23-MAY-1997; US-047594.
PR 23-MAY-1997; US-047595.
PR 23-MAY-1997; US-047596.
PR 23-MAY-1997; US-047597.
PR 23-MAY-1997; US-047598.
PR 23-MAY-1997; US-047599.
PR 23-MAY-1997; US-047600.
PR 23-MAY-1997; US-047601.
PR 23-MAY-1997; US-047612.
PR 23-MAY-1997; US-047613.
PR 23-MAY-1997; US-047614.
PR 23-MAY-1997; US-047615.
PR 23-MAY-1997; US-047617.
PR 23-MAY-1997; US-047618.
PR 23-MAY-1997; US-047632.
PR 23-MAY-1997; US-047633.
PR 06-JUN-1997; US-048964.
PR 06-JUN-1997; US-048974.
PR 13-JUN-1997; US-049610.
PR 08-JUL-1997; US-051926.
PR 16-JUL-1997; US-052874.
PR 18-AUG-1997; US-055724.
PR 22-AUG-1997; US-056630.
PR 22-AUG-1997; US-056631.
PR 22-AUG-1997; US-056632.
PR 22-AUG-1997; US-056636.
PR 22-AUG-1997; US-056637.
PR 22-AUG-1997; US-056662.
PR 22-AUG-1997; US-056664.
PR 22-AUG-1997; US-056845.
PR 22-AUG-1997; US-056862.
PR 22-AUG-1997; US-056864.
PR 22-AUG-1997; US-056872.
PR 22-AUG-1997; US-056874.
PR 22-AUG-1997; US-056875.
PR 22-AUG-1997; US-056876.
PR 22-AUG-1997; US-056877.
PR 22-AUG-1997; US-056878.
PR 22-AUG-1997; US-056879.
PR 22-AUG-1997; US-056880.
PR 22-AUG-1997; US-056881.
PR 22-AUG-1997; US-056882.
PR 22-AUG-1997; US-056884.
PR 22-AUG-1997; US-056886.
PR 22-AUG-1997; US-056887.
PR 22-AUG-1997; US-056888.
PR 22-AUG-1997; US-056889.
PR 22-AUG-1997; US-056892.
PR 22-AUG-1997; US-056893.
PR 22-AUG-1997; US-056894.
PR 22-AUG-1997; US-056903.
PR 22-AUG-1997; US-056908.
PR 22-AUG-1997; US-056909.
PR 22-AUG-1997; US-056910.
PR 22-AUG-1997; US-056911.
PR 05-SEP-1997; US-057650.
PR 05-SEP-1997; US-057669.
PR 05-SEP-1997; US-057761.
PR 12-SEP-1997; US-058785.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
DR WPI; 98-506364/43.
DR P-PSDB; W74848.
PT New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim 1; Page 353-354; 721pp; English.
CC This sequence represents a nucleic acid molecule designated Gene 120 from
CC the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and ATCC
CC 209048) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. V59502) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also, pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on

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PR   11-FEB-1997; US-798897.
PR   25-NOV-1997; US-978523.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 99-214150/18.
DR   P-PSDB; W97392.
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
PS   Disclosure; Columns 15-16; 26pp; English.
CC   The present sequence encodes human bcl-y protein (Hbcl-y). The
CC   specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
SQ   Sequence   579 BP;    106 A;    154 C;    208 G;    111 T;

  Query Match             85.6%;  Score 497.4;  DB 1;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 1.2e-124;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db       1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db      61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
           || |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db     121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db     181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db     241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db     301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
           ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db     361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy     421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
           ||||| |||||||||||| |||||||||||||||||||||||||||||||||||| || |||
Db     421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
           |||||||||||||| |||||||||| |||||| |||||||||||||||||||||||||||
Db     481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy     541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db     541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT  11
V41925
ID   V41925 standard; cDNA; 1098 BP.
AC   V41925;
DT   20-NOV-1998  (first entry)
DE   Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .1098
FT                   /*tag=  a
FT                   /product= "Bcl-like (HAICH29) protein"
PN   WO9831800-A2.
PD   23-JUL-1998.
PF   21-JAN-1998; U00960.
PR   21-JAN-1997; US-034205.
PR   21-JAN-1997; US-034204.
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
PI   Su JY;
DR   WPI; 98-414099/35.
DR   P-PSDB; W59884.
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
PS   Claim 2; Fig 12A-12D; 120pp; English.
CC   This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
SQ   Sequence   1098 BP;    264 A;    279 C;    325 G;    230 T;

  Query Match             62.8%;  Score 364.8;  DB 1;  Length 1098;
  Best Local Similarity   90.3%;  Pred. No. 5.2e-89;
  Matches  390;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db       1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db      61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db     121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
           |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db     181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
           ||||| ||||| |||||||| |||||||||||| |||||||||||| ||||| || ||||||
Db     241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db     301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
           ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db     361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420
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  Query Match            86.2%;  Score 501;  DB 1;  Length 583;
  Best Local Similarity  91.4%;  Pred. No. 1.3e-125;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db    241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   9
V28334
ID   V28334 standard; cDNA; 579 BP.
AC   V28334;
DT   02-OCT-1998  (first entry)
DE   Human bcl-y gene.
KW   ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .579
FT                   /*tag= a
FT                   /product= bcl-y
FT                   /note= "No stop codon given"
PN   US5789201-A.
PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   P-PSDB; W61392.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Claim 3; Column 15/16; 27pp; English.
CC   The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC   family, components in the cell death pathway.  The bcl-2 family
CC   have both apoptotic activity and the apoptosis blocking activity.  bcl-y
CC   falls in the apoptosis activity category.  The  recombinant protein may
CC   be used to prevent uncontrolled cell growth, either by its direct
CC   administration to recombinant genetic constructs to increase its
CC   expression in vivo.  Also, antisense constructs can be used in disorders
CC   where prevention of cell death is desired.
SQ   Sequence   579 BP;    106 A;    154 C;    208 G;    111 T;


  Query Match            85.6%;  Score 497.4;  DB 1;  Length 579;
  Best Local Similarity  91.2%;  Pred. No. 1.2e-124;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          || |||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db    241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT  10
X15946
ID   X15946 standard; cDNA; 579 BP.
AC   X15946;
DT   20-MAY-1999  (first entry)
DE   cDNA encoding the human bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite; ss.
OS   Homo sapiens.
PN   US5883229-A.
PD   16-MAR-1999.
PF   25-NOV-1997; 978523.
PR   23-FEB-1996; US-012201.
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Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||| |||||||||| |||||||||||||||||||||||||||||||||||||||| || |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   7
T96577
ID   T96577 standard; DNA; 583 BP.
AC   T96577;
DT   22-APR-1998  (first entry)
DE   Human bcl-w DNA.
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .582
FT                   /*tag= a
FT                   /product= bcl-w
PN   WO9735971-A1.
PD   02-OCT-1997.
PF   27-MAR-1997; AU0199.
PR   27-MAR-1996; AU-008965.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR   WPI; 97-489635/45.
DR   P-PSDB; W36047.
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
PS   Claim 3; Page 48; 86pp; English.
CC   This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
CC   family, extracted from an adult brain library. This gene promotes cell
CC   survival, so its modulation is useful in treatment of cancer or
CC   auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
CC   disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
CC   human immunodeficiency virus infection or in cell transplants.
CC   Up-regulation of the gene can also be used to modify cell lines cultured
CC   in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC   and to increase survival of primary explants during genetic modification.
CC   It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC   antibody production or screening of potential modulators.
SQ   Sequence   583 BP;    105 A;    157 C;    210 G;    111 T;


  Query Match             86.2%;  Score 501;  DB 1;  Length 583;
  Best Local Similarity   91.4%;  Pred. No. 1.3e-125;
  Matches  531;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
            ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          |||||||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    241 CAGGTCTCCGACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
          |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||| || ||||  ||||||||||||||||
Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGTCGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          |||||||||||||| |||||||||| |||||| |||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   8
X25134
ID   X25134 standard; DNA; 583 BP.
AC   X25134;
DT   05-JUL-1999  (first entry)
DE   Human bcl-w gene derivative.
KW   Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW   animal model; ss.
OS   Homo sapiens.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   P-PSDB; Y05532.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Disclosure; Page 36; 52pp; English.
CC   The present sequence is described as a derivative of the human
CC   bcl-w gene (see X25132) and encodes Bcl-w protein (see Y05532), a
CC   pro-survival member of the Bcl-2 family which is widely expressed
CC   and which is essential for spermatogenesis.  The invention relates
CC   generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for
CC   inducing or reducing fertility of male animals.  Methods are
CC   provided for the treatment of infertility, or for reducing
CC   fertility, by modulating spermatogenesis.  An animal model carries
CC   a mutation is at least one allele of the human or murine bcl-w gene
CC   or in a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   583 BP;    105 A;    157 C;    210 G;    111 T;
```

KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite; ss.
OS Rattus sp.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
DR P-PSDB; W97391.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 13-16; 26pp; English.
CC The present sequence encodes rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;

Query Match 93.0%; Score 540.6; DB 1; Length 579;
Best Local Similarity 95.9%; Pred. No. 3.2e-136;
Matches 555; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db       1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
           | |||||| ||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Db      61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
           |||||||||||||||||||||| |||||||||||||||||||||||| ||||| ||||||
Db     121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
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Db     241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db     361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy     421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db     421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
           |||||||||||||| |||||||||| |||||| |||||| |||||||||| |||||||||
Db     481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy     541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db     541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT 6
X25132
ID X25132 standard; DNA; 581 BP.
AC X25132;
DT 05-JUL-1999 (first entry)
DE Human bcl-w gene.
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
KW animal model; ss.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR P-PSDB; Y05530.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Claim 3; Page 32; 52pp; English.
CC The present sequence is the human bcl-w gene encoding Bcl-w protein
CC (see Y05530), a pro-survival member of the Bcl-2 family which is
CC widely expressed and which is essential for spermatogenesis. The
CC invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male
CC animals. Methods are provided for the treatment of infertility, or
CC for reducing fertility, by modulating spermatogenesis. An animal
CC model carries a mutation is at least one allele of the human or
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals
CC have disorganised seminferous tubules and are substantially
CC infertile, but possess no other major abnormalities as determined
CC by histological examination. They can be used to screen for
CC therapeutic molecules including genetic sequences capable of
CC inducing, enhancing or otherwise facilitating spermatogenesis in
CC animals, or which can induce infertility.
SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T;

Query Match 86.5%; Score 502.6; DB 1; Length 581;
Best Local Similarity 91.6%; Pred. No. 5e-126;
Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db       1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
           | |||||||||||||||||||||||||||||| || ||||| |||||||| || |||
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Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db     121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db     181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
           ||||| ||||| |||||||| |||||||||||| |||||||||||| ||||| || ||||||
Db     241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
```

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CC   have disorganised seminferous tubules and are substantially
CC   infertile, but possess no other major abnormalities as determined
CC   by histological examination.  They can be used to screen for
CC   therapeutic molecules including genetic sequences capable of
CC   inducing, enhancing or otherwise facilitating spermatogenesis in
CC   animals, or which can induce infertility.
SQ   Sequence   581 BP;    106 A;    158 C;    200 G;    117 T;


  Query Match            96.4%;  Score 560.2;  DB 1;  Length 581;
  Best Local Similarity  97.8%;  Pred. No. 1.8e-141;
  Matches  568;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   4
V28333
ID   V28333 standard; cDNA; 579 BP.
AC   V28333;
DT   02-OCT-1998  (first entry)
DE   Rat bcl-y gene.
KW   ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS   Rattus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .579
FT                   /*tag= a
FT                   /product= bcl-y
FT                   /note= "No stop codon given"
PN   US5789201-A.
PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   P-PSDB; W61391.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Claim 2; Column 13/14; 27pp; English.
CC   The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC   family, components in the cell death pathway.  The bcl-2 family
CC   have both apoptotic activity and the apoptosis blocking activity.  bcl-y
CC   falls in the apoptosis activity category.  The  recombinant protein may
CC   be used to prevent uncontrolled cell growth, either by its direct
CC   administration to recombinant genetic constructs to increase its
CC   expression in vivo.  Also, antisense constructs can be used in disorders
CC   where prevention of cell death is desired.
SQ   Sequence   579 BP;    111 A;    157 C;    198 G;    113 T;


  Query Match            93.0%;  Score 540.6;  DB 1;  Length 579;
  Best Local Similarity  95.9%;  Pred. No. 3.2e-136;
  Matches  555;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||
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Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          |||||||||||||||||||||| |||||||||||||||||||||| ||||| ||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

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          |||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT   5
X15945
ID   X15945 standard; cDNA; 579 BP.
AC   X15945;
DT   20-MAY-1999  (first entry)
DE   cDNA encoding the rat bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   2
X25135
ID   X25135 standard; DNA; 581 BP.
AC   X25135;
DT   05-JUL-1999  (first entry)
DE   Mouse bcl-w gene derivative.
KW   Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW   animal model; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .507
FT                   /*tag=  a
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   P-PSDB; Y05533.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Disclosure; Page 38; 52pp; English.
CC   The present sequence is described as a derivative of the mouse
CC   bcl-w gene (see X25133) and encodes Bcl-w protein (see Y05533), a
CC   pro-survival member of the Bcl-2 family which is widely expressed
CC   and which is essential for spermatogenesis.  The invention relates
CC   generally to a method of treatment and to an animal model for the
CC   identification of molecules and genetic sequences useful for
CC   inducing or reducing fertility of male animals.  Methods are
CC   provided for the treatment of infertility, or for reducing
CC   fertility, by modulating spermatogenesis.  An animal model carries
CC   a mutation is at least one allele of the human or murine bcl-w gene
CC   or in a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   581 BP;    105 A;    164 C;    195 G;    117 T;


  Query Match            100.0%;  Score 581;  DB 1;  Length 581;
  Best Local Similarity  100.0%;  Pred. No. 4.7e-147;

  Matches  581;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGCAACTGGGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   3
X25133
ID   X25133 standard; DNA; 581 BP.
AC   X25133;
DT   05-JUL-1999  (first entry)
DE   Mouse bcl-w gene.
KW   Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
KW   animal model; ss.
OS   Mus sp.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   P-PSDB; Y05531.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Claim 3; Page 34; 52pp; English.
CC   The present sequence is the mouse bcl-w gene encoding Bcl-w protein
CC   (see Y05531), a pro-survival member of the Bcl-2 family which is
CC   widely expressed and which is essential for spermatogenesis.  The
CC   invention relates generally to a method of treatment and to an
CC   animal model for the identification of molecules and genetic
CC   sequences useful for inducing or reducing fertility of male
CC   animals.  Methods are provided for the treatment of infertility, or
CC   for reducing fertility, by modulating spermatogenesis.  An animal
CC   model carries a mutation is at least one allele of the human or
CC   murine bcl-w gene or in a gene associated with bcl-w.  Such animals
```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2000, 01:26:24 ; Search time 115.05 Seconds
(without alignments)
1263.465 Million cell updates/sec

Title: US-09-155-327B-8
Perfect score: 581
Sequence: 1 atgccgaccccagcctcaac.....gccttttttgctagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	581	100.0	581	1	T96578	Mouse bcl-w DNA. N
2	581	100.0	581	1	X25135	Mouse bcl-w gene d
3	560.2	96.4	581	1	X25133	Mouse bcl-w gene.
4	540.6	93.0	579	1	V28333	Rat bcl-y gene. Nu
5	540.6	93.0	579	1	X15945	cDNA encoding the
6	502.6	86.5	581	1	X25132	Human bcl-w gene.
7	501	86.2	583	1	T96577	Human bcl-w DNA. N
8	501	86.2	583	1	X25134	Human bcl-w gene d
9	497.4	85.6	579	1	V28334	Human bcl-y gene.
10	497.4	85.6	579	1	X15946	cDNA encoding the
11	364.8	62.8	1098	1	V41925	Nucleotide sequenc
12	364.4	62.7	1864	1	V59630	Human secreted pro
13	134.6	23.2	926	1	Q81698	Human thymus BCL-X
14	134.6	23.2	926	1	T40079	Bcl-XL gene. Induc
15	134.6	23.2	7372	1	X33182	Base sequence of t
16	125	21.5	765	1	Q49815	Bcl-2. Treating tu
17	125	21.5	953	1	X33183	Bcl-2 DNA fragment
18	125	21.5	5086	1	Q54631	Human oncogene bcl
19	125	21.5	5086	1	Q86661	Human bcl-2 gene.
20	125	21.5	5105	1	N81292	Sequence of bcl-2
21	125	21.5	7996	1	X33184	Base sequence of t
22	123.4	21.2	760	1	T33694	Human BCL2 cDNA. S
23	120.2	20.7	1274	1	Q81696	Chicken lymphoid B
24	119	20.5	615	1	Q73987	Human bcl-2 gene O
25	119	20.5	911	1	X08431	bcl-2 proto-oncoge
26	115.8	19.9	831	1	N81293	Sequence of bcl-2
27	113.8	19.6	1384	1	V17638	Mouse BCL-x gamma
28	57	9.8	737	1	Q81699	Human thymus BCL-X
29	44.4	7.6	5408	1	Q95494	Human Cdn-3 DNA. N
30	40.6	7.0	624	1	Q97606	Human Bax protein
31	40.6	7.0	624	1	V84005	cDNA encoding a hu
32	39.4	6.8	822	1	T48488	Bax omega protein
33	37.6	6.5	1286	1	T42139	Bak-2 gene. Screen
34	37.6	6.5	6511	1	Q95493	Human Cdn-2 DNA. N
c 35	37	6.4	3855	1	Q13287	P.denitrificans ge
36	36.4	6.3	1968	1	T17375	Bcl-Y cDNA. New is
37	36.4	6.3	2072	1	Q95492	Human Cdn-1 cDNA.
38	36.4	6.3	2094	1	T42138	Bak gene. Screenin
39	36.4	6.3	2094	1	V61498	Bak cDNA. New Bak-
c 40	35.2	6.1	509	1	V89057	EST clone CB239. N
41	34.4	5.9	494	1	V44433	Mycobacterium tube
42	34.4	5.9	494	1	V64542	M. tuberculosis im
c 43	33.8	5.8	11531	1	Q54222	BSSL/CEL Gene. DNA
44	33.8	5.8	114955	1	X53491	Human adenosine A1
c 45	33.6	5.8	496	1	X01131	M. tuberculosis an

ALIGNMENTS

RESULT 1
T96578
ID T96578 standard; DNA; 581 BP.
AC T96578;
DT 22-APR-1998 (first entry)
DE Mouse bcl-w DNA.
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 1. .507
FT /*tag= a
FT /product= bcl-w
FT /note= "q"
PN WO9735971-A1.
PD 02-OCT-1997.
PF 27-MAR-1997; AU0199.
PR 27-MAR-1996; AU-008965.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR WPI; 97-489635/45.
DR P-PSDB; W36048.
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
PS Claim 3; Page 50-51; 86pp; English.
CC This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
CC family. This gene promotes cell survival, so its modulation is useful in
CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.
CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,
CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell
CC transplants. Up-regulation of the gene can also be used to modify cell
CC lines cultured in vivo, e.g. to develop new lines, to facilitate
CC isolation of hybridomas and to increase survival of primary explants
CC during genetic modification. It can be used to produce recombinant Bcl-w
CC for therapy, diagnosis, antibody production or screening of potential
CC modulators.
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T;

Query Match 100.0%; Score 581; DB 1; Length 581;
Best Local Similarity 100.0%; Pred. No. 4.7e-147;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Db      1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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DR   N-PSDB; Q81698.
PT   New poly-nucleotide encoding new poly-peptide(s) that modify
PT   apoptosis - and related vectors, recombinant cells and
PT   antibodies, useful in assay and for control of cell death in e.g.
PT   neuronal cells, lymphocytes and cancers
PS   Claim 3; Page 94; 127pp; English.
CC   This protein may be expressed recombinantly, particularly with pcmV
CC   plasmids as vectors for expression in mammalian cell cultures.  The
CC   protein has particular application in cancer cells (failure of
CC   programmed cell death (PCD)) or neurodegenerative and autoimmune
CC   diseases (premature PCD), e.g. Parkinson's disease, amylotrophic
CC   lateral sclerosis and multiple sclerosis.
SQ   Sequence   233 AA;

  Query Match           44.1%;  Score 616;  DB 1;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 7.90e-47;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
            ||:||| |||:|||: ||:::  || :||: :|  ||: :|||  |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT   15
ID   W05821 standard; Protein; 233 AA.
AC   W05821;
DT   30-MAR-1997  (first entry)
DE   Bcl-XL protein.
KW   Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
KW   Bcl-2 homology domain; gene therapy; HIV; AIDS; antisense;
KW   immune disorder; autoimmune disease; graft rejection;
KW   graft-versus-host disease; apoptosis; adoptive immunotherapy.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   domain          129. .148
FT                   /note= "BH1 domain"
FT   domain          180. .191
FT                   /note= "BH2 domain"
PN   WO9634956-A1.
PD   07-NOV-1996.
PF   02-MAY-1996; U06203.
PR   04-MAY-1995; US-435518.
PR   07-JUN-1995; US-481739.
PA   (ARCH-) ARCH DEV CORP.
PA   (USNA ) US SEC OF NAVY.
PI   June CH,  Thompson CB;
DR   WPI; 96-506159/50.
DR   N-PSDB; T40079.
PT   Inducing or preventing death of T cells by bcl-XL protein regulation
PT   - used to increase survival of HIV infected cells or to
PT   down:regulate immune responses in immune diseases
PS   Disclosure; Page 52-53; 76pp; English.
CC   This is the sequence of a human bcl-XL protein, which protects
CC   T-lymphocytes against cell death.  A splice variant form, bcl-XS,
CC   lacks a stretch of 63 amino acids, and is a dominant negative
CC   regulator of bcl-XL function.  The gene may be modified to
CC   facilitate interaction with costimulatory Bax protein and inhibit
CC   interaction with antagonistic Bad protein, by modification of the
CC   Bcl-2 homology domains BH1 and/or BH2.  The bcl-XL gene may be
CC   introduced into T-cells in vivo or ex vivo via gene transfer using
CC   a vector for HIV infection gene therapy, to augment intracellular
CC   bcl-XL protein levels and protect from cell death.  A corresponding
CC   antisense oligonucleotide or expression vector may be used in gene
CC   therapy of e.g. autoimmune disease, graft rejection or graft-
CC   versus-host disease, to induce cell death (e.g. apoptosis) and
CC   down-regulate the immune response in a T-lymphocyte population.
SQ   Sequence   233 AA;

  Query Match           44.1%;  Score 616;  DB 1;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 7.90e-47;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
            ||:||| |||:|||: ||:::  || :||: :|  ||: :|||  |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


Search completed: Fri Jun 23 14:13:45 2000
Job time : 14 secs.
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CC   Such animals have disorganised seminferous tubules and are
CC   substantially infertile, but possess no other major abnormalities
CC   as determined by histological examination.  They can be used to
CC   screen for therapeutic molecules including genetic sequences
CC   capable of inducing, enhancing or otherwise facilitating
CC   spermatogenesis in animals, or which can induce infertility.
SQ   Sequence   192 AA;

  Query Match           95.3%;  Score 1331;  DB 1;  Length 192;
  Best Local Similarity  93.8%;  Pred. No. 6.54e-117;
  Matches   181;  Conservative    9;  Mismatches   2;  Indels   1;  Gaps   1;

Db       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||:|||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179
           |||:|:|||||||| |||||||||:||||||||||:|||||||||| | ||:||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db     180 GALVTVGAFFASK 192
           |||||||||||||
Qy     181 GALVTVGAFFASK 193


RESULT   12
ID   W36048 standard; Protein; 168 AA.
AC   W36048;
DT   22-APR-1998  (first entry)
DE   Mouse bcl-w protein.
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease.
OS   Mus sp.
PN   WO9735971-A1.
PD   02-OCT-1997.
PF   27-MAR-1997; AU0199.
PR   27-MAR-1996; AU-008965.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR   WPI; 97-489635/45.
DR   N-PSDB; T96578.
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
PS   Claim 6; Page 50-51; 86pp; English.
CC   This sequence represents a novel protein, bcl-w, encoded by the mouse
CC   bcl-2 gene family. This gene promotes cell survival, so its modulation
CC   is useful in treatment of cancer or auto-immune diseases, degenerative
CC   diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC   degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC   or in cell transplants. Up-regulation of the gene can also be used to
CC   modify cell lines cultured in vivo, e.g. to develop new lines, to
CC   facilitate isolation of hybridomas and to increase survival of primary
CC   explants during genetic modification. It can be used to produce
CC   recombinant Bcl-w for therapy, diagnosis, antibody production or
CC   screening of potential modulators.
SQ   Sequence   168 AA;

  Query Match           86.0%;  Score 1202;  DB 1;  Length 168;
  Best Local Similarity  94.6%;  Pred. No. 3.67e-104;
  Matches   159;  Conservative    8;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||:|||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
           |||:|:|||||||| |||||||||:||||||||||:|||||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168


RESULT   13
ID   W59884 standard; Protein; 365 AA.
AC   W59884;
DT   20-NOV-1998  (first entry)
DE   Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent.
OS   Homo sapiens.
PN   WO9831800-A2.
PD   23-JUL-1998.
PF   21-JAN-1998; U00960.
PR   21-JAN-1997; US-034205.
PR   21-JAN-1997; US-034204.
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
PI   Su JY;
DR   WPI; 98-414099/35.
DR   N-PSDB; V41925.
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
PS   Claim 1; Fig 12A-12D; 120pp; English.
CC   This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
SQ   Sequence   365 AA;

  Query Match           75.1%;  Score 1049;  DB 1;  Length 365;
  Best Local Similarity  98.6%;  Pred. No. 4.39e-89;
  Matches   142;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGW 144
           |||||||||||||| |||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGW 144


RESULT   14
ID   R68887 standard; Protein; 233 AA.
AC   R68887;
DT   10-AUG-1995  (first entry)
DE   Human thymus BCL-XL.
KW   BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;
KW   autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
KW   multiple sclerosis.
OS   Homo sapiens.
PN   WO9500642-A.
PD   05-JAN-1995.
PF   22-JUN-1994; U07089.
PR   22-JUN-1993; US-081448.
PA   (ARCH-) ARCH DEV CORP.
PA   (UNMI ) UNIV MICHIGAN.
PI   Boise LH,  Nunez G,  Thompson CB;
DR   WPI; 95-052079/07.
```

PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Claim 2; Columns 19-22; 26pp; English.
CC The present sequence represents a mammalian bcy-l protein.
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain
CC viable in culture for an extended period. In contrast, if they act as
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC conditions associated with prolonged cell life span such as cancer
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC diseases. They may also be used to cause cell death in, and hence
CC control, parasites.
SQ Sequence 192 AA;

Query Match 97.9%; Score 1368; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.42e-120;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Db      1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db    121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    182 ALVTVGAFFASK 193
```

RESULT 10
ID W97393 standard; Protein; 192 AA.
AC W97393;
DT 20-MAY-1999 (first entry)
DE Protein sequence of the specification.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
OS Unidentified.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 19-20; 26pp; English.
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain
CC viable in culture for an extended period. In contrast, if they act as
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC conditions associated with prolonged cell life span such as cancer
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC diseases. They may also be used to cause cell death in, and hence
CC control, parasites.
SQ Sequence 192 AA;

Query Match 97.9%; Score 1367; DB 1; Length 192;
Best Local Similarity 97.4%; Pred. No. 1.79e-120;
Matches 187; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Db      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db    121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    182 ALVTVGAFFASK 193
```

RESULT 11
ID Y05533 standard; Protein; 192 AA.
AC Y05533;
DT 05-JUL-1999 (first entry)
DE Mouse Bcl-w protein deritvative.
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
OS Mus sp.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR N-PSDB; X25135.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 39; 52pp; English.
CC The present sequence is described of a derivative of mouse Bcl-w
CC (see also Y05531), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.

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          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193
```

RESULT 7
ID W97391 standard; Protein; 193 AA.
AC W97391;
DT 20-MAY-1999 (first entry)
DE The rat bcl-y protein.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
OS Rattus sp.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
DR N-PSDB; X15945.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Disclosure; Columns 15-18; 26pp; English.
CC The present sequence represents rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
SQ Sequence 193 AA;

Query Match 98.6%; Score 1378; DB 1; Length 193;
Best Local Similarity 97.4%; Pred. No. 1.46e-121;
Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193
```

RESULT 8
ID W61391 standard; Protein; 193 AA.
AC W61391;
DT 02-OCT-1998 (first entry)
DE Rat bcl-y protein.
KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS Rattus sp.
PN US5789201-A.
PD 04-AUG-1998.
PF 11-FEB-1997; 798897.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 98-446079/38.
DR N-PSDB; V283333.
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontrolled cell
PT growth e.g. cancers
PS Example; Fig 3A; 27pp; English.
CC The mammalian bcl-y protein is a member of the bcl-2 family, components
CC in the cell death pathway. The bcl-2 family have both apoptotic activity
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC activity category. The recombinant protein may be used to prevent
CC uncontrolled cell growth, either by its direct administration to
CC recombinant genetic constructs to increase its expression in vivo. Also,
CC antisense constructs can be used in disorders where prevention of cell
CC death is desired.
SQ Sequence 193 AA;

Query Match 98.6%; Score 1378; DB 1; Length 193;
Best Local Similarity 97.4%; Pred. No. 1.46e-121;
Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193
```

RESULT 9
ID W97394 standard; Protein; 192 AA.
AC W97394;
DT 20-MAY-1999 (first entry)
DE Mammalian bcl-y protein.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
OS Mammalia.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.

```
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see X25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   193 AA;

  Query Match           98.8%;  Score 1380;  DB 1;  Length 193;
  Best Local Similarity  97.9%;  Pred. No. 9.23e-122;
  Matches   189;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     181 GALVTVGAFFASK 193


RESULT    5
ID   W61392 standard; Protein; 193 AA.
AC   W61392;
DT   02-OCT-1998  (first entry)
DE   Human bcl-y protein.
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS   Homo sapiens.
PN   US5789201-A.
PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   N-PSDB; V28334.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Example; Column 17/18; 27pp; English.
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway.  The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity.  bcl-y falls in the apoptosis
CC   activity category.  The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo.  Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
SQ   Sequence   193 AA;

  Query Match           98.7%;  Score 1379;  DB 1;  Length 193;
  Best Local Similarity  98.4%;  Pred. No. 1.16e-121;
  Matches   190;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     181 GALVTVGAFFASK 193


RESULT    6
ID   W97392 standard; Protein; 193 AA.
AC   W97392;
DT   20-MAY-1999  (first entry)
DE   The human bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
OS   Homo sapiens.
PN   US5883229-A.
PD   16-MAR-1999.
PF   25-NOV-1997; 978523.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PR   25-NOV-1997; US-978523.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 99-214150/18.
DR   N-PSDB; X15946.
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
PS   Claim 1; Columns 17-18; 26pp; English.
CC   The present sequence represents human bcl-y protein (Hbcl-y). The
CC   specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
SQ   Sequence   193 AA;

  Query Match           98.7%;  Score 1379;  DB 1;  Length 193;
  Best Local Similarity  98.4%;  Pred. No. 1.16e-121;
  Matches   190;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
```

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Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193


RESULT    2
ID   W36047 standard; Protein; 193 AA.
AC   W36047;
DT   22-APR-1998  (first entry)
DE   Human bcl-w protein.
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease.
OS   Homo sapiens.
PN   WO9735971-A1.
PD   02-OCT-1997.
PF   27-MAR-1997; AU0199.
PR   27-MAR-1996; AU-008965.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR   WPI; 97-489635/45.
DR   N-PSDB; T96577.
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
PS   Claim 6; Page 48; 86pp; English.
CC   This sequence represents a novel human protein, bcl-w, encoded by the
CC   bcl-2 gene family and extracted from an adult brain library. This gene
CC   promotes cell survival, so its modulation is useful in treatment of
CC   cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC   Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC   ischaemia, human immunodeficiency virus infection or in cell transplants.
CC   Up-regulation of the gene can also be used to modify cell lines cultured
CC   in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC   and to increase survival of primary explants during genetic modification.
CC   It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC   antibody production or screening of potential modulators.
SQ   Sequence   193 AA;

  Query Match           100.0%;  Score 1397;  DB 1;  Length 193;
  Best Local Similarity 100.0%;  Pred. No. 1.91e-123;
  Matches   193;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193


RESULT    3
ID   Y05530 standard; Protein; 193 AA.
AC   Y05530;
DT   05-JUL-1999  (first entry)
DE   Human Bcl-w protein essential for spermatogenesis.
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
OS   Homo sapiens.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   N-PSDB; X25132.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Claim 2; Page 33; 52pp; English.
CC   The present sequence is human Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see X25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   193 AA;

  Query Match           99.0%;  Score 1383;  DB 1;  Length 193;
  Best Local Similarity 99.0%;  Pred. No. 4.66e-122;
  Matches   191;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

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Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193


RESULT    4
ID   Y05531 standard; Protein; 193 AA.
AC   Y05531;
DT   05-JUL-1999  (first entry)
DE   Mouse Bcl-w protein essential for spermatogenesis.
KW   Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW   animal model.
OS   Mus sp.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   N-PSDB; X25133.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Claim 2; Page 35; 52pp; English.
CC   The present sequence is mouse Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:13:31 2000; MasPar time 7.29 Seconds
626.869 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 32.637; Variance 140.214; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1397	100.0	193	1	Y05532	Human Bcl-w protein es	1.91e-123
2	1397	100.0	193	1	W36047	Human bcl-w protein.	1.91e-123
3	1383	99.0	193	1	Y05530	Human Bcl-w protein es	4.66e-122
4	1380	98.8	193	1	Y05531	Mouse Bcl-w protein es	9.23e-122
5	1379	98.7	193	1	W61392	Human bcl-y protein.	1.16e-121
6	1379	98.7	193	1	W97392	The human bcl-y protei	1.16e-121
7	1378	98.6	193	1	W97391	The rat bcl-y protein.	1.46e-121
8	1378	98.6	193	1	W61391	Rat bcl-y protein.	1.46e-121
9	1368	97.9	192	1	W97394	Mammalian bcl-y protei	1.42e-120
10	1367	97.9	192	1	W97393	Protein sequence of th	1.79e-120
11	1331	95.3	192	1	Y05533	Mouse Bcl-w protein de	6.54e-117
12	1202	86.0	168	1	W36048	Mouse bcl-w protein.	3.67e-104
13	1049	75.1	365	1	W59884	Amino acid sequence of	4.39e-89
14	616	44.1	233	1	R68887	Human thymus BCL-XL.	7.90e-47
15	616	44.1	233	1	W05821	Bcl-XL protein.	7.90e-47
16	616	44.1	233	1	W31530	Human anti-apoptotic B	7.90e-47
17	615	44.0	225	1	W19396	"Deprenyl" (RTM)-induc	9.87e-47
18	586	41.9	239	1	W87810	A human Bcl-2 protein.	6.14e-44
19	575	41.2	239	1	W87812	A human Bcl-2-alpha pr	7.02e-43
20	575	41.2	239	1	R71404	Human bcl-2 alpha prot	7.02e-43
21	575	41.2	239	1	R70331	Human bcl-2 protein.	7.02e-43
22	575	41.2	239	1	R42312	Bcl-2 oncogene product	7.02e-43
23	575	41.2	239	1	W40217	Human bcl-2.	7.02e-43
24	575	41.2	239	1	P80987	Sequence of bcl-2-alph	7.02e-43
25	575	41.2	239	1	R47344	Human oncogene bcl-2 p	7.02e-43
26	572	40.9	232	1	W01019	Apoptosis-blocking pro	1.36e-42
27	572	40.9	232	1	W94346	Human Bcl-2 mutant pro	1.36e-42
28	572	40.9	236	1	W87811	A murine Bcl-2 protein	1.36e-42
29	572	40.9	239	1	W94345	Human Bcl-2 wild-type	1.36e-42
30	572	40.9	239	1	W01018	Apoptosis-blocking pro	1.36e-42
31	565	40.4	232	1	W01020	Apoptosis-blocking pro	6.42e-42
32	565	40.4	232	1	W94347	Human Bcl-2 mutant pro	6.42e-42
33	561	40.2	239	1	W02383	Human BCL2.	1.55e-41
34	537	38.4	190	1	R68884	Chicken lymphoid BCL-X	3.12e-39
35	535	38.3	235	1	W48312	Mouse BCL-x gamma.	4.84e-39
36	499	35.7	205	1	R68886	Human thymus BCL-2.	1.34e-35
37	499	35.7	205	1	W31529	Human anti-apoptotic B	1.34e-35
38	499	35.7	205	1	W87813	A human Bcl-2-beta pro	1.34e-35
39	499	35.7	205	1	R71405	Human bcl-2 beta prote	1.34e-35
40	499	35.7	205	1	R70332	Human bcl-2 protein.	1.34e-35
41	499	35.7	205	1	W96319	bcl-2 polypeptide.	1.34e-35
42	467	33.4	205	1	P80988	Sequence of bcl-2-beta	1.49e-32
43	448	32.1	229	1	W94348	Human Bcl-2 mutant pro	9.46e-31
44	448	32.1	229	1	W01021	Apoptosis-blocking pro	9.46e-31
45	333	23.8	63	1	R68885	Human thymus BCL-X1.	5.77e-20

ALIGNMENTS

RESULT 1
ID Y05532 standard; Protein; 193 AA.
AC Y05532;
DT 05-JUL-1999 (first entry)
DE Human Bcl-w protein essential for spermatogenesis.
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR N-PSDB; X25134.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 37; 52pp; English.
CC The present sequence is described of a derivative of human Bcl-w
CC (see also Y05530), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
SQ Sequence 193 AA;

Query Match 100.0%; Score 1397; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.91e-123;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 56.8%; Pred. No. 7.9e-21;
Matches 249; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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Qy      98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
           || ||||||      |    |   |  || | |||||  || |||  || || |||||||
Db     242 CCCGGGAGGTGATCCCCATGGCTGCAGTGAAGCAAGCGCTGAGGGAGGCGGGCGATGAGT 301

Qy     158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
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Qy     218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaagggggccccaact 277
           |  ||||  | ||  ||||    |||||     ||||||| || |  |  ||    ||||
Db     362 GGACAGCGTATCAGAGCTTTGAGCAGGTAGTGAACGAACTCTTCCGGGATGGGGTGAACT 421

Qy     278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
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Db     422 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGTGGGGCACTGTGCGTGGAGAGCGTAGACA 481

Qy     338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
           |||||||| |   | ||||| | |   |       |||||||   | |||||| |    |
Db     482 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAACTTGGATGGCCACTTACCTGAATGACC 541

Qy     398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
             || |     ||||||||    |  || |||||||     ||    |  || |||||
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Qy     458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
           ||   ||    |  |||  |||      | |||| |   |     ||   |  ||| |
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Search completed: July 4, 2000, 01:21:54
Job time: 16595 sec

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Qy    521 tgacgggggccgtggcact 539
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Db    672 TGACTGTGGCTGGTGTAGT 690


RESULT  14
S76513
LOCUS       S76513        726 bp    mRNA            ROD       26-SEP-1995
DEFINITION  bcl-x=apoptosis inhibitor [protooncogene] [rats, ovary, mRNA
            Partial, 726 nt].
ACCESSION   S76513
VERSION     S76513.1  GI:998481
KEYWORDS    .
SOURCE      Rattus sp. ovary.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Tilly,J.L., Tilly,K.I., Kenton,M.L. and Johnson,A.L.
  TITLE     Expression of members of the bcl-2 gene family in the immature rat
            ovary: equine chorionic gonadotropin-mediated inhibition of
            granulosa cell apoptosis is associated with decreased bax and
            constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels
  JOURNAL   Endocrinology 136 (1), 232-241 (1995)
  MEDLINE   95129487
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 162917] from the original journal article.
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                     /db_xref="taxon:10118"
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                     FELRYRRAFSDLTSQLHITPGTVYQSFEQVVNELFRDGVNWGRIVASSSFGGALCVES
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BASE COUNT      181 a    177 c    220 g    148 t
ORIGIN


  Query Match             23.7%;  Score 138.2;  DB 12;  Length 726;
  Best Local Similarity   57.2%;  Pred. No. 2.1e-21;
  Matches  251;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

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Db    312 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 371

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaactggg 280
          |||   | ||  ||||    |||||     | ||||| |||| |  ||    |||||||
Db    372 CAGTATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 431

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| |||| ||    ||||||||  ||||||||  |   || || ||  ||||||
Db    432 GTCGCATTGTGGCCTCCTCCTCCTTTGGGGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 491

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          |||||  |   | ||||| | |   |       |||||||   ||||||||  |    |  |
Db    492 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 551

Qy    401 tggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacggggacg 460
          | |     ||||||||     |  || |||||||     ||    | ||| ||||||  ||
Db    552 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACA 611

Qy    461 gggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacagtgc 520
          |      |||   |||     | |||| |    |     |   |   |||  |
Db    612 ATACAGCACCCGAGAGCCGGAAAGGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCA 671

Qy    521 tgacgggggccgtggcact 539
          |||| | ||| |   | | |
Db    672 TGACTGTGGCTGGTGTAGT 690


RESULT  15
AF216205
LOCUS       AF216205      720 bp    mRNA            MAM       11-FEB-2000
DEFINITION  Sus scrofa anti-apoptotic regulator Bcl-xL (bcl-xL) mRNA, complete
            cds.
ACCESSION   AF216205
VERSION     AF216205.1  GI:6959766
KEYWORDS    .
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Lee,T.L. and Canty,J.M.
  TITLE     PCR Cloning of a Porcine bcl-xL cDNA from Heart
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Lee,T.L. and Canty,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main
            Street, Buffalo, NY 14214-3000, USA
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /tissue_type="heart"
     gene            1. .720
                     /gene="bcl-xL"
     CDS             13. .714
                     /gene="bcl-xL"
                     /codon_start=1
                     /product="anti-apoptotic regulator Bcl-xL"
                     /protein_id="AAF33212.1"
                     /db_xref="GI:6959767"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
                     AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
                     TLAGVVLLGSLFSRK"
BASE COUNT      170 a    176 c    229 g    145 t
ORIGIN


  Query Match             23.3%;  Score 135.6;  DB 3;  Length 720;
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  JOURNAL   Unpublished
FEATURES             Location/Qualifiers
     source          1. .2232
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /dev_stage="embryonic"
                     /tissue_type="brain"
                     /clone_lib="hippocampal cDNA libr. and genomic DNA libr."
                     /clone="X9, X31"
     5'UTR           <1. .19
     gene            20. .721
                     /gene="bcl-x"
     CDS             20. .721
                     /gene="bcl-x"
                     /codon_start=1
                     /protein_id="CAA57886.1"
                     /db_xref="GI:607177"
                     /db_xref="SWISS-PROT:P53563"
                     /translation="MSQSNQELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
                     RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
                     TVAGVVLLGSLFSRK"
     CDS             join(20. .394,584. .721)
                     /gene="bcl-x"
                     /note="smaller form due to splicing"
                     /codon_start=1
                     /protein_id="CAA57887.1"
                     /db_xref="GI:607178"
                     /db_xref="SWISS-PROT:P53563"
                     /translation="MSQSNQELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
                     RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGV
                     VLLGSLFSRK"
     3'UTR           722. .2232
     polyA_signal    2184. .2189
BASE COUNT      479 a    646 c    602 g    505 t
ORIGIN


  Query Match             24.5%;  Score 143;  DB 12;  Length 2232;
  Best Local Similarity   57.9%;  Pred. No. 1.6e-22;
  Matches  254;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||      |    |   |  || | |||||  || | |  |||||  |||||||| |
Db    252 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 311

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | |||||  ||| | ||||||||
Db    312 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 371

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaactggg 280
          ||||  | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    372 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 431

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| ||||||||   |||||| |  |||||||| |  || || ||  ||||||
Db    432 GTCGCATTGTGGCCTTCTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 491

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          ||||| |   | ||||| | |   |        |||||||   |||||||| |     |  |
Db    492 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 551

Qy    401 tggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacggggacg 460
          | |     ||||||||     |  || |||||||     ||     | ||| ||||||  ||
Db    552 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACA 611

Qy    461 gggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacagtgc 520
            ||    |  |||   |||       | |||| |   |       |   |   ||| |
Db    612 ATGCAGCAGCCGAGAGCCGGAAAGGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCA 671

Qy    521 tgacgggggccgtggcact 539
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          |||| | ||| |  | | |
Db    672 TGACTGTGGCTGGTGTAGT 690


RESULT  13
RNU34963
LOCUS       RNU34963      726 bp    mRNA            ROD       02-OCT-1995
DEFINITION  Rattus norvegicus programmed cell death repressor BCL-X-Long mRNA,
            complete cds.
ACCESSION   U34963
VERSION     U34963.1  GI:1004376
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Tilly,J.L., Tilly,K.I., Kenton,M.L. and Johnson,A.L.
  TITLE     Expression of members of the bcl-2 gene family in the immature rat
            ovary: equine chorionic gonadotropin-mediated inhibition of
            granulosa cell apoptosis is associated with decreased bax and
            constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels
  JOURNAL   Endocrinology 136 (1), 232-241 (1995)
  MEDLINE   95129487
REFERENCE   2  (bases 1 to 726)
  AUTHORS   Tilly,J.L., Tilly,K.I., Kenton,M.L. and Johnson,A.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-1995) Jonathan L. Tilly, Department of Obstetrics
            and Gynecology/Vincent Center for Reproductive Biology,
            Massachusetts General Hospital/Harvard Medical School, 32 Fruit
            Street, Boston, MA 02114, USA
FEATURES             Location/Qualifiers
     source          1. .726
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="ovary"
     CDS             20. .721
                     /note="programmed cell death repressor; Bcl-2 homolog;
                     long isoform of BCL-X; member of the bcl-2 gene family"
                     /codon_start=1
                     /product="BCL-X-Long"
                     /protein_id="AAA77686.1"
                     /db_xref="GI:1004377"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
                     RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVLPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTVYQSFEQVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQ
                     VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGM
                     TVAGVVLLGSLFSRK"
BASE COUNT      181 a    177 c    220 g    148 t
ORIGIN


  Query Match             23.7%;  Score 138.2;  DB 12;  Length 726;
  Best Local Similarity   57.2%;  Pred. No. 2.1e-21;
  Matches  251;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||  |   |     |   |  || | |||||  || | |  |||||  |||||||| |
Db    252 GGGAGGTACTCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 311

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | |||||  ||| | ||||||||
Db    312 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 371

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaactggg 280
          |||   | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    372 CAGTATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 431

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| |||| ||    ||||||||  ||||||||  |  || || ||  ||||||
Db    432 GTCGCATTGTGGCCTCCTCCTCCTTTGGGGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 491
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                     /codon_start=1
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                     /protein_id="AAA19257.1"
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                     RETPSAINGNPSWHLADSPEVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
                     TVAGVVLLGSLFSRK"
BASE COUNT      192 a    187 c    229 g    156 t
ORIGIN


  Query Match             24.5%;  Score 143;  DB 12;  Length 764;
  Best Local Similarity   57.9%;  Pred. No. 1.8e-22;
  Matches  254;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||      |    |   |  || | |||||  || | |  ||||| ||||||||| |
Db    271 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 330

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | |||||  ||| | |||||||||
Db    331 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 390

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggcccccaactggg 280
          ||||  | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    391 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 450

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| ||||||||   |||||| |  |||||||| |  || || ||  ||||||
Db    451 GTCGCATTGTGGCCTTCTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 510

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          |||||  |   | |||| | |   |       |||||||  ||||||||  |    |  |
Db    511 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 570

Qy    401 tggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacggggacg 460
          | |     ||||||||     |  || |||||||      ||     | ||| |||||| ||
Db    571 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACA 630

Qy    461 gggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacagtgc 520
            ||    |  |||   |||      | |||| |   |      |   |  ||| |
Db    631 ATGCAGCAGCCGAGAGCCGGAAAGGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCA 690

Qy    521 tgacgggggccgtggcact 539
          |||| | ||| |  | | |
Db    691 TGACTGTGGCTGGTGTAGT 709


RESULT  11
RNU72350
LOCUS       RNU72350     1742 bp    mRNA            ROD       22-OCT-1996
DEFINITION  Rattus norvegicus Bcl-xalpha mRNA, complete cds.
ACCESSION   U72350
VERSION     U72350.1  GI:1622936
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1742)
  AUTHORS   Shiraiwa,N., Inohara,N., Okada,S., Yuzaki,M., Shoji,S. and Ohta,S.
  TITLE     An additional form of rat Bcl-x, Bcl-xbeta, generated by an
            unspliced RNA, promotes apoptosis in promyeloid cells
  JOURNAL   J. Biol. Chem. 271 (22), 13258-13265 (1996)
  MEDLINE   96278736
REFERENCE   2  (bases 1 to 1742)
  AUTHORS   Shiraiwa,N., Inohara,N., Okada,S., Yuzaki,M., Shoji,S. and Ohta,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1996) Division of Biochemistry, Institute of
            Gerontology, 1-396 Kosugi-cho, Nakahara-ku, Kawasaki City 211,
            Japan

FEATURES             Location/Qualifiers
     source          1. .1742
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             72. .773
                     /codon_start=1
                     /product="Bcl-xalpha"
                     /protein_id="AAB17353.1"
                     /db_xref="GI:1622937"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
                     RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
                     TVAGVVLLGSLFSRK"
BASE COUNT      377 a    507 c    477 g    381 t
ORIGIN


  Query Match             24.5%;  Score 143;  DB 12;  Length 1742;
  Best Local Similarity   57.9%;  Pred. No. 1.6e-22;
  Matches  254;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||      |    |   |  || | |||||  || | |  ||||| ||||||||| |
Db    304 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 363

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | |||||  ||| | |||||||||
Db    364 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 423

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggcccccaactggg 280
          ||||  | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    424 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 483

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| ||||||||   |||||| |  |||||||| |  || || ||  ||||||
Db    484 GTCGCATTGTGGCCTTCTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 543

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          |||||  |   | |||| | |   |       |||||||  ||||||||  |    |  |
Db    544 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 603

Qy    401 tggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacggggacg 460
          | |     ||||||||     |  || |||||||      ||     | ||| |||||| ||
Db    604 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACA 663

Qy    461 gggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacagtgc 520
            ||    |  |||   |||      | |||| |   |      |   |  ||| |
Db    664 ATGCAGCAGCCGAGAGCCGGAAAGGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCA 723

Qy    521 tgacgggggccgtggcact 539
          |||| | ||| |  | | |
Db    724 TGACTGTGGCTGGTGTAGT 742


RESULT  12
RNCBLXLS
LOCUS       RNCBLXLS     2232 bp    DNA             ROD       31-DEC-1994
DEFINITION  R.norvegicus bcl-x gene.
ACCESSION   X82537
VERSION     X82537.1  GI:607176
KEYWORDS    bcl-x gene.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 2232)
  AUTHORS   Michaelidis,T.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1994) T.M. Michaelidis, Max-Planck-Inst. for
            Psychiatry, Dept of Neurochemistry, 82152 Martinsried, FRG
REFERENCE   2  (bases 1 to 2232)
  AUTHORS   Michaelidis,T.M.
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Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Db  90001 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 90060

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  90061 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 90120

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Db  90121 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 90180

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||||||||||||||||||||||||||||| |||||  ||||||||||||||||
Db  90181 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 90240

Qy    421 agtgggggctggg 433
          |||||||||||||
Db  90241 AGTGGGGGCTGGG 90253
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RESULT   9
XLR1
LOCUS       XLR1          749 bp    mRNA            VRT       01-JUL-1997
DEFINITION  X.laevis R1 mRNA.
ACCESSION   X82462
VERSION     X82462.1  GI:575421
KEYWORDS    xR1 gene.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
            Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   Cruz-Reyes,J. and Tata,J.R.
  TITLE     Cloning, characterization and expression of two Xenopus bcl-2-like
            cell-survival genes
  JOURNAL   Gene 158 (2), 171-179 (1995)
  MEDLINE   95331613
REFERENCE   2  (bases 1 to 749)
  AUTHORS   Cruz-Reyes,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
            Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
            1AA, UK
FEATURES             Location/Qualifiers
     source          1. .749
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /dev_stage="28-30 (tailbud tadpole)"
                     /clone_lib="lambda ZapII:R1"
                     /clone="pKS+:xR1"
     gene            3. .689
                     /gene="xR1"
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                     /note="Protein sequence is in conflict with the conceptual
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                     /db_xref="SWISS-PROT:Q91827"
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                     IHVTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDW
                     MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL
                     MTVGALFASK"
BASE COUNT      203 a    146 c    224 g    176 t
ORIGIN
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  Query Match             40.9%;  Score 238.2;  DB 4;  Length 749;
  Best Local Similarity   65.3%;  Pred. No. 9.3e-44;
  Matches  370;  Conservative    0;  Mismatches  188;  Indels    9;  Gaps    1;

Qy     16 tcggccccagacacacgggctctggtggcagactttgtaggttataagctgaggcagaag 75
          || | || ||   | ||||||| |||| |  || || ||  | || ||| |  | |||
Db    132 TCTGACCTAGGATCCCGGGCTTTGGTAGAGGATTTGGTGAGGTACAAGTTATGCCAGCGT 191

Qy     76 ggttatgtctgtggagctggccccggggagggcccagcagctgacccgctgcaccaagcc 135
          ||   ||    |   ||           ||  ||||| |     |  ||||    ||
Db    192 AGTCTGGTTCCGGAGCCT---------TCAGGAGCAGCATCCTGTGCTTTGCATTCGGCT 242

Qy    136 atgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctgatctggcg 195
          ||||| || || || ||||| || |||   || ||| | |   | |||  |||  |  |
Db    243 ATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCATTCAGTGAGATCTCC 302

Qy    196 gctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccaggtctccgacgaa 255
          | ||| | ||||||||||| ||| ||||  |   ||||||  |  | ||  | |
Db    303 ACACAGATCCATGTGACCCCCGGCACAGCATATGCACGCTTTGCAGAAGTAGCAGGTAGC 362

Qy    256 ctttttcaaggggggccccaactggggccgccttgtagccttctttctctttggggctgca 315
          || || ||||| ||    || ||||| ||| | || || || ||| | ||||| || ||
Db    363 CTATTCCAAGGTGGGGTGAATTGGGGTCGCATAGTTGCATTTTTTGTTTTTGGTGCCGCG 422

Qy    316 ctgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtgg 375
          |||||||||||||||||||||||||||||    || ||  ||  ||   | || || |||
Db    423 CTGTGTGCTGAGAGTGTCAACAAGGAGATGTCCCCTCTTCTGCCACGGATCCAAGACTGG 482

Qy    376 atggtggcctacctggagacgcggctggtcgactggatccacagcagtgggggctgggcg 435
          |||||| | || ||||||||    |||   |||||||| || |||| ||| ||||||
Db    483 ATGGTGACATATCTGGAGACAAACCTGAGAGACTGGATTCAGAGCAATGGTGGCTGGAAT 542

Qy    436 gagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcgggagggg 495
          | |||   | ||||||| ||||| || ||| | || || ||  || | |  || ||||||
Db    543 GGGTTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGGAGGCAACGTGAGGGG 602

Qy    496 aactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggtaact 555
          || ||||||||| ||| ||| ||  | || || || ||||| ||||| ||  || | ||
Db    603 AATTGGGCATCACTGAAGACTGTCTTAACTGGAGCTGTGGCTCTGGGTGCTTTGATGACA 662

Qy    556 gtaggggccttttttgctagcaagtga 582
          |||||||||||| ||||| |||||||||
Db    663 GTAGGGGCCTTGTTTGCCAGCAAGTGA 689
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```
RESULT  10
RNU10579
LOCUS       RNU10579      764 bp    DNA             ROD       26-JUN-1994
DEFINITION  Rattus norvegicus Bcl-x (bcl-x) gene, complete cds.
ACCESSION   U10579
VERSION     U10579.1  GI:505698
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   Wesselingh,S.L., David,G.L., Choi,S., Veliuona,M. and Hardwick,J.M.
  TITLE     Cloning and expression of rat bcl-x in cultured neurons
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 764)
  AUTHORS   Hardwick,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins
            School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681,
            USA
FEATURES             Location/Qualifiers
     source          1. .764
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /tissue_type="brain"
     gene            39. .740
                     /gene="bcl-x"
     CDS             39. .740
                     /gene="bcl-x"
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Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    299 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 358

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    359 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 418

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    419 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 478

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          |||||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    479 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 538

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||| |||||||||||||||||||| || ||||  ||||||||||||||||
Db    539 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 598

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    599 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 658

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 718

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
          |||||||||||||||||||||||||||||||||||||||||||
Db    719 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 760
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RESULT   8
CNS0000B
LOCUS       CNS0000B   196287 bp    DNA             PRI       27-OCT-1999
DEFINITION  Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
            RPCI-11 library from chromosome 14 of Homo sapiens (Human),
            complete sequence.
ACCESSION   AL049829
VERSION     AL049829.3  GI:6138746
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 196287)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     On Oct 28, 1999 this sequence version replaced gi:4972127.
            IMPORTANT: This sequence is unfinished and does not necessarly
            represent the correct sequence. Work on the sequence is in progress
            and the release of this data is based on the understanding that the
            sequence may change as work continue. The sequence may be
            contaminated with foreign sequence from E.coli, yeast, vector,
            phage, etc.XX.
FEATURES             Location/Qualifiers
     source          1. .196287
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone_lib="RPCI-11"
                     /clone="R-124D2"
     STS             78257. .78396
                     /standard_name="AA908790"
                     /note="matching EMBL:AA908790; Identified using the e-PCR
                     software (G. Schuler)"
     STS             80431. .80564
                     /standard_name="AA167748"
                     /note="matching EMBL:AA167748; Identified using the e-PCR
                     software (G. Schuler)"
     STS             82162. .82297
                     /standard_name="H79035"
                     /note="matching EMBL:H79035; Identified using the e-PCR
                     software (G. Schuler)"
     STS             93575. .93803
                     /standard_name="AA007328"
                     /note="matching EMBL:AA007328; Identified using the e-PCR
                     software (G. Schuler)"
     STS             107753. .107946
                     /standard_name="R94929"
                     /note="matching EMBL:R94929; Identified using the e-PCR
                     software (G. Schuler)"
     STS             107991. .108176
                     /standard_name="D11677"
                     /note="matching EMBL:D11677; Identified using the e-PCR
                     software (G. Schuler)"
     STS             128383. .128521
                     /standard_name="H22648"
                     /note="matching EMBL:H22648; Identified using the e-PCR
                     software (G. Schuler)"
     STS             128415. .128539
                     /standard_name="R87257"
                     /note="matching EMBL:R87257; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138457. .138733
                     /standard_name="R59134"
                     /note="matching EMBL:R59134; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138504. .138653
                     /standard_name="M78864"
                     /note="matching EMBL:M78864; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138563. .138642
                     /standard_name="M78986"
                     /note="matching EMBL:M78986; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138563. .138672
                     /standard_name="M78946"
                     /note="matching EMBL:M78946; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138800. .138921
                     /standard_name="H72023"
                     /note="matching EMBL:H72023; Identified using the e-PCR
                     software (G. Schuler)"
     STS             161612. .161756
                     /standard_name="AA452257"
                     /note="matching EMBL:AA452257; Identified using the e-PCR
                     software (G. Schuler)"
     STS             194799. .194898
                     /standard_name="N91549"
                     /note="matching EMBL:N91549; Identified using the e-PCR
                     software (G. Schuler)"
BASE COUNT    50873 a  45668 c  47123 g  52623 t
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  Query Match             72.6%;  Score 423.4;  DB 10;  Length 196287;
  Best Local Similarity   98.6%;  Pred. No. 2.1e-85;
  Matches  427;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  89821 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 89880

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  89881 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 89940

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  89941 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 90000
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  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="14"
                     /cell_line="BaF3"
     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
                     /gene="bcl-w"
                     /note="promotes cell survival; Bcl-2 homolog"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAB09056.1"
                     /db_xref="GI:1572495"
                     /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
                     GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
BASE COUNT      107 a    158 c    200 g    117 t
ORIGIN
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  Query Match             89.7%;  Score 522.8;  DB 12;  Length 582;
  Best Local Similarity   93.6%;  Pred. No. 2.4e-107;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||  |||||||||||||||||| ||||| |||||||||||| |||
Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          |||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
          |||||||||||| |||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          |||||||||| |||||||||||||||||||| || |||| ||||||||||||||||
Db    361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
          |||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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RESULT   7
AF030769
LOCUS       AF030769     3476 bp    mRNA            ROD       16-NOV-1997
DEFINITION  Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION   AF030769
VERSION     AF030769.1  GI:2623249
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3476)
  AUTHORS   Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
            MacGregor,G.R.
  TITLE     Bcl-w is required for testis homeostasis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3476)
  AUTHORS   Ross,A.J. and MacGregor,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
            University, 1462 Clifton Road, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
     source          1. .3476
                     /organism="Mus musculus"
                     /strain="C57BL/10J"
                     /db_xref="taxon:10090"
                     /chromosome="14"
                     /map="19.5 cM"
     gene            1. .3476
                     /gene="Bcl-w"
     exon            1. .82
                     /gene="Bcl-w"
                     /number=1
     exon            83. .170
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                     /number=2
     exon            171. .610
                     /gene="Bcl-w"
                     /number=3
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                     /product="BCL-W"
                     /protein_id="AAB86430.1"
                     /db_xref="GI:2623250"
                     /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
     exon            611. .3476
                     /gene="Bcl-w"
                     /number=4
     misc_feature    3356. .3364
                     /gene="Bcl-w"
                     /note="mRNA destabilization element"
     polyA_signal    3428. .3441
                     /gene="Bcl-w"
BASE COUNT      796 a    814 c    991 g    875 t
ORIGIN
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  Best Local Similarity   93.6%;  Pred. No. 2e-107;
  Matches  545;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          ||||||||||||||||  |||||||||||||||||| ||||| |||||||||||| |||
Db    179 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 238

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          |||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db    239 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 298
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     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
                     /gene="bcl-w"
                     /note="Bcl-2 family member"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAC64200.1"
                     /db_xref="GI:3747130"
                     /translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
                     GAALCAESVNKEMEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
BASE COUNT      111 a    157 c    200 g    114 t
ORIGIN


  Query Match             90.5%;  Score 527.6;  DB 12;  Length 582;
  Best Local Similarity   94.2%;  Pred. No. 2e-108;
  Matches  548;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
          |||||||||||||||  |||||||||||||||||| ||||| |||||||||||| |||
Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          |||||||| |||||||||||||||||||||||||||||| ||||| |||||||||||| |||
Db     61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||
Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          |||||  ||||||||||||||  |||||||||||||||||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
          ||||||||||| |||||||| |||||||||||||| ||  |||  ||||||||||||||||
Db    361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
          |||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582


RESULT   5
AR020779
LOCUS       AR020779      579 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 1 from patent US 5789201.
ACCESSION   AR020779
VERSION     AR020779.1  GI:3975394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Guastella,J.
  TITLE     Genes coding for bcl-y a bcl-2 homologue
  JOURNAL   Patent: US 5789201-A 1 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="unknown"
BASE COUNT      111 a    157 c    198 g    113 t
ORIGIN


  Query Match             89.7%;  Score 523;  DB 5;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 2.1e-107;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

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Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Db     61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          |||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
          |||||  ||||||||||||||  |||||||||||||||||||||||| ||||| || ||||||
Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT   6
MMU59746
LOCUS       MMU59746      582 bp    mRNA            ROD       29-SEP-1996
DEFINITION  Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59746
VERSION     U59746.1  GI:1572494
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
REFERENCE   2  (bases 1 to 582)
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ORIGIN


  Query Match             98.6%;  Score 575;  DB 9;  Length 3542;
  Best Local Similarity   99.1%;  Pred. No. 4.2e-119;
  Matches  578;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttcttt 300
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Db    417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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Db    537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

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RESULT   3
AR020780
LOCUS       AR020780      579 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 2 from patent US 5789201.
ACCESSION   AR020780
VERSION     AR020780.1  GI:3975395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Guastella,J.
  TITLE     Genes coding for bcl-y a bcl-2 homologue
  JOURNAL   Patent: US 5789201-A 2 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .579
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Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy    241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttcttt 300
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Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Qy    361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
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Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT   4
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LOCUS       AF096291      582 bp    mRNA            ROD       15-OCT-1998
DEFINITION  Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   AF096291
VERSION     AF096291.1  GI:3747129
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Differential expression of Bcl-w and Bcl-x mRNA in the developing
            and adult nervous system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
            University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES             Location/Qualifiers
     source          1. .582
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LOCUS       HSU59747      582 bp    mRNA            PRI       29-SEP-1996
DEFINITION  Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59747
VERSION     U59747.1  GI:1572492
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
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     CDS             1. .582
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ORIGIN
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Query Match 99.0%; Score 577.2; DB 10; Length 582;
Best Local Similarity 99.5%; Pred. No. 1.6e-119;
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    241 caggtctccgacgaacttttttcaaggggggccccaactggggccgccttgtagccttcttt 300
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Qy    301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
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RESULT  2
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LOCUS       D87461       3542 bp    mRNA            PRI       10-JUL-1997
DEFINITION  Human mRNA for KIAA0271 gene, complete cds.
ACCESSION   D87461
VERSION     D87461.1  GI:1944417
KEYWORDS    KIAA0271.
SOURCE      Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA,
            clone_lib:pSPORT 1 clone:HA6752.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3542)
  AUTHORS   Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo
            Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3
            Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
REFERENCE   2  (sites)
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes.VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from human cell line KG-1 and brain
  JOURNAL   Unpublished (1996)
REFERENCE   3  (sites)
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
  MEDLINE   97191544
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                     /clone="HA6752"
                     /clone_lib="pSPORT 1"
                     /sex="male"
                     /tissue_type="brain"
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 20:45:19 ; Search time 888.39 Seconds
(without alignments)
-638.388 Million cell updates/sec

Title: US-09-155-327B-6
Perfect score: 583
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	577.2	99.0	582	10	HSU59747	U59747 Human Bcl-w
	2	575	98.6	3542	9	D87461	D87461 Human mRNA
	3	567.8	97.4	579	5	AR020780	AR020780 Sequence
	4	527.6	90.5	582	12	AF096291	AF096291 Rattus no
	5	523	89.7	579	5	AR020779	AR020779 Sequence
	6	522.8	89.7	582	12	MMU59746	U59746 Mus musculu
	7	522.8	89.7	3476	12	AF030769	AF030769 Mus muscu
	8	423.4	72.6	196287	10	CNS0000B	AL049829 Human chr
	9	238.2	40.9	749	4	XLR1	X82462 X.laevis R1
	10	143	24.5	764	12	RNU10579	U10579 Rattus norv
	11	143	24.5	1742	12	RNU72350	U72350 Rattus norv
	12	143	24.5	2232	12	RNCBLXLS	X82537 R.norvegicu
	13	138.2	23.7	726	12	RNU34963	U34963 Rattus norv
	14	138.2	23.7	726	12	S76513	S76513 bcl-x=apopt
	15	135.6	23.3	720	3	AF216205	AF216205 Sus scrof
	16	135.6	23.3	752	3	SSJ001203	AJ001203 Sus scrof
	17	132.8	22.8	699	12	MMBCLXL	X83574 M.musculus
	18	132.8	22.8	702	12	MMU10101	U10101 Mus musculu
	19	132.8	22.8	979	12	MUSBCLX	L35049 Mus musculu
	20	132.8	22.8	1466	12	MMU51278	U51278 Mus musculu
	21	132.8	22.8	5771	14	AF060226	AF060226 Eukaryoti
	22	131	22.5	926	5	AR054021	AR054021 Sequence
	23	131	22.5	926	5	I52011	I52011 Sequence 5
	24	131	22.5	926	9	HSBCLXL	Z23115 H.sapiens b
	25	129.8	22.3	1748	12	RNU72349	U72349 Rattus norv
	26	128.6	22.1	708	12	RNU34964	U34964 Rattus norv
	27	128.2	22.0	687	3	BTU92434	U92434 Bos taurus
	28	127	21.8	1179	12	RATBCL2A	L14680 Rattus norv
	29	127	21.8	1184	4	GGU26645	U26645 Gallus gall
	30	123.4	21.2	717	5	AR052622	AR052622 Sequence
	31	123.4	21.2	765	5	A76121	A76121 Sequence 1
	32	123.4	21.2	5086	5	AR052621	AR052621 Sequence
	33	123.4	21.2	5086	5	AR054008	AR054008 Sequence
	34	123.4	21.2	5086	9	HUMBCL2A	M13994 Human B-cel
	35	123.4	21.2	5105	5	I08038	I08038 Sequence 1
	36	123.2	21.1	723	10	HSU72398	U72398 Human Bcl-x
c	37	123.2	21.1	74673	42	AC016218	AC016218 Homo sapi
	38	123.2	21.1	151029	33	HSJ857M17	AL117381 Homo sapi
	39	122.8	21.1	1684	4	CHKBCL1	D11381 Gallus gall
	40	121.8	20.9	760	5	AR021160	AR021160 Sequence
	41	121.8	20.9	6030	9	HUMBCL2C	M14745 Human bcl-2
	42	120.6	20.7	2914	12	MUSBCL21	M16506 Mouse bcl-2
	43	120.4	20.7	1384	12	MMU51277	U51277 Mus musculu
	44	120.2	20.6	1235	12	MMU10102	U10102 Mus musculu
	45	120.2	20.6	1846	5	AR054009	AR054009 Sequence

ALIGNMENTS

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Qy     451 tacgg 455
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Db    2062 TACGG 2066
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Search completed: July 4, 2000, 01:24:21
Job time: 14809 sec

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Db   1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy    271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
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Db   1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy    331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
          ||||||  |||||||   || |||||||   |  |      |||||||   |  ||||||
Db   1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy    391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
           |   ||  |||  |  |||||||||    |  || |||||||  |  ||    |  ||
Db   2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy    451 tacgg 455
          |||||
Db   2062 TACGG 2066


RESULT 14
PCT-US93-05651-4
; Sequence 4, Application PC/TUS9305651
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  A Gene Which Prevents Programmed Cell Death
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  diskette
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/05651
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1459..2178
;      OTHER INFORMATION:  /product= "Bcl-2"
PCT-US93-05651-4


  Query Match             21.2%;  Score 123.4;  DB 6;  Length 5086;
  Best Local Similarity   58.6%;  Pred. No. 8.2e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |       | | ||||  ||| | ||   ||| ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| ||| ||  |||| | ||  || |    ||||||||  ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || ||    |  ||
Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
           ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||   |  ||||||
Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
           |   ||  |||  |  |||||||||    |  || |||||||  |  ||    |  ||
Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
          |||||
Db    2062 TACGG 2066


RESULT 15
PCT-US93-06251-2
; Sequence 2, Application PC/TUS9306251
;  GENERAL INFORMATION:
;    APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;    TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;    TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06251
;      FILING DATE:  19930630
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-2


  Query Match             21.2%;  Score 123.4;  DB 6;  Length 5086;
  Best Local Similarity   58.6%;  Pred. No. 8.2e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |       | | ||||  ||| | ||   ||| ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
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Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || ||    |  ||
Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
           ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||   |  ||||||
Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
           |   ||  |||  |  |||||||||    |  || |||||||  |  ||    |  ||
Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061
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; Patent No. 5834306
;  GENERAL INFORMATION:
;    APPLICANT:  Webster, Keith A.
;    APPLICANT:  Bishopric, Nanette H.
;    TITLE OF INVENTION:  Tissue Specific Hypoxia Regulated
;    TITLE OF INVENTION:  Therapeutic Constructs
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/365,486A
;      FILING DATE:  23-DEC-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  8255-0018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  human bcl-2 cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1459..2178
US-08-365-486A-14


  Query Match             21.2%;  Score 123.4;  DB 3;  Length 5086;
  Best Local Similarity   58.6%;  Pred. No. 8.2e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |      | | ||||  ||| | ||   ||| ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| |||  ||  |||| | ||  || |    |||||||  ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggc 270
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Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
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Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
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Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
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Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
           |||||
Db    2062 TACGG 2066


RESULT  13
US-09-080-285-19
; Sequence 19, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-080-285-19


  Query Match             21.2%;  Score 123.4;  DB 5;  Length 5086;
  Best Local Similarity   58.6%;  Pred. No. 8.2e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
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Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| |||  ||  |||| | ||  || |    |||||||  ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggc 270
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Qy    451 tacgg 455
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Db    604 TACGG 608


RESULT 10
5459251-1
;Patent No. 5459251
;    APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.
;    TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
;SEQUENCES
;    NUMBER OF SEQUENCES: 4
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/228,704
;      FILING DATE: 18-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 994,941
;      FILING DATE: 23-DEC-1992
;      APPLICATION NUMBER: 663,010
;      FILING DATE: 19-MAR-1991
;      APPLICATION NUMBER: 883,687
;      FILING DATE: 09-JUL-1986
;SEQ ID NO:1:
;      LENGTH: 4825
5459251-1


  Query Match             21.2%;  Score 123.4;  DB 7;  Length 4825;
  Best Local Similarity   58.6%;  Pred. No. 8e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |      | | ||||  ||| | ||   ||| ||
Db    1702 gcggggcctgcgctcagcccggtgccacctgtggtccacctggccctccgccaagccggc 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
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Db    1762 gacgacttctcccgccgctaccgcggcgacttcgccgagatgtccagccagctgcacctg 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggc 270
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Db    1822 acgcccttcaccgcgcggggacgctttgccacggtggtggaggagctcttcagggacggg 1881

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
           ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db    1882 gtgaactgggggaggattgtggccttctttgagttcggtggggtcatgtgtgtggagagc 1941

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||   |  ||||||
Db    1942 gtcaaccgggagatgtcgcccctggtggacaacatcgccctgtggatgactgagtacctg 2001

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
           |   ||  |||  |  |||||||||    |  || |||||||  |  ||    |  ||
Db    2002 aaccggcacctgcacacctggatccaggataacggaggctgggatgcctttgtggaactg 2061

Qy     451 tacgg 455
           |||||
Db    2062 tacgg 2066


RESULT 11
US-08-465-485A-19
; Sequence 19, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-465-485A-19


  Query Match             21.2%;  Score 123.4;  DB 3;  Length 5086;
  Best Local Similarity   58.6%;  Pred. No. 8.2e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |      | | ||||  ||| | ||   ||| ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| |||  ||  |||| | ||  || |    |||||||  ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || ||    |  ||
Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
           ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||   |  ||||||
Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
           |   ||  |||  |  |||||||||    |  || |||||||  |  ||    |  ||
Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
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Db    2062 TACGG 2066


RESULT 12
US-08-365-486A-14
; Sequence 14, Application US/08365486A
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;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..717
US-08-465-485A-20


  Query Match             21.2%;  Score 123.4;  DB 3;  Length 717;
  Best Local Similarity   58.6%;  Pred. No. 4.8e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |      | | ||||  ||| | ||   ||| ||
Db     244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| ||| || |||| | ||  || |    |||||||| ||
Db     304 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 363

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || ||    |  ||
Db     364 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 423

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
             ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db     424 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 483

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||  |  ||||||
Db     484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
             |   ||  |||  |  |||||||||     |  || |||||||  |  ||     |  ||
Db     544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603

Qy     451 tacgg 455
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Db     604 TACGG 608


RESULT   9
US-09-080-285-20
; Sequence 20, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..717
US-09-080-285-20


  Query Match             21.2%;  Score 123.4;  DB 5;  Length 717;
  Best Local Similarity   58.6%;  Pred. No. 4.8e-23;
  Matches  214;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy      91 gctggccccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctgga 150
           || || || | |    |||| |   |      | | ||||  ||| | ||   ||| ||
Db     244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303

Qy     151 gatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtg 210
           || || |||     ||||| ||| || |||| | ||  || |    |||||||| ||
Db     304 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 363

Qy     211 accccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || ||    |  ||
Db     364 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 423

Qy     271 cccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagt 330
             ||||||||  |  |||| |||||||||   || || |  |   ||||||  |||||
Db     424 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 483

Qy     331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
           ||||||  |||||||   || |||||||   |  |      |||||||  |  ||||||
Db     484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543

Qy     391 gagacgcggctggtcgactggatccacagcagtgggggctgggcggagttcacagctcta 450
             |   ||  |||  |  |||||||||     |  || |||||||  |  ||     |  ||
Db     544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603
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  Query Match             22.5%;  Score 131;  DB 3;  Length 926;
  Best Local Similarity   56.3%;  Pred. No. 6e-25;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy      98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
           || ||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db     364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy     158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
           | ||    || | ||||||  | |||  ||| ||| |  | ||||| ||  | |||||||
Db     424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy     218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggggccccaact 277
           |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db     484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy     278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
           |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db     544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy     338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
           |||||||| |   | ||||| | |   |    |  |||||||   | ||||||  |    |
Db     604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy     398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
             || |     ||||||||     |  || |||||||     ||    |  || || |||
Db     664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy     458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
           ||   ||    |  |||   ||       | |||  |   |     |   |  ||| |
Db     724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

Qy     518 tgctgacggggccg 532
              |||| | |||||
Db     784 GCATGACTGTGGCCG 798


RESULT   7
PCT-US94-07089-6
; Sequence 6, Application PC/TUS9407089
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
;    TITLE OF INVENTION:  Compositions and Methods
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS, ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07089
;      FILING DATE:  CONCURRENTLY FILED
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/081.448
;      FILING DATE:  22 JUNE 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARKER, David L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  ARCD090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  713-789-2679
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
PCT-US94-07089-6


  Query Match             22.5%;  Score 131;  DB 6;  Length 926;
  Best Local Similarity   56.3%;  Pred. No. 6e-25;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy      98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
           || ||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db     364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy     158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
           | ||    || | ||||||  | |||  ||| ||| |  | ||||| ||  | |||||||
Db     424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy     218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggggccccaact 277
           |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db     484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy     278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
           |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db     544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy     338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
           |||||||| |   | ||||| | |   |    |  |||||||   | ||||||  |    |
Db     604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy     398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
             || |     ||||||||     |  || |||||||     ||    |  || || |||
Db     664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy     458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
           ||   ||    |  |||   ||       | |||  |   |     |   |  ||| |
Db     724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

Qy     518 tgctgacggggccg 532
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Db     784 GCATGACTGTGGCCG 798


RESULT   8
US-08-465-485A-20
; Sequence 20, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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Qy    421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT   5
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Craig B.
;    APPLICANT:  Boise, Lawrence H.
;    TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
;    TITLE OF INVENTION:  Compositions and Methods
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  321 No. 5646008th Clark Street, Suite 800
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/081,448
;      FILING DATE:  19930622
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5646008thrup, Thomas E.
;      REGISTRATION NUMBER:  33,268
;      REFERENCE/DOCKET NUMBER:  ARCD090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-744-0090
;      TELEFAX:  312-755-4489
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-081-448-5


  Query Match             22.5%;  Score 131;  DB 1;  Length 926;
  Best Local Similarity   56.3%;  Pred. No. 6e-25;
  Matches  245;  Conservative    0;  Mismatches  190;  Indels    0;  Gaps    0;

Qy     98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
          || |||||||      |    |   |  |  | |||||  || |||  || || || ||||
Db    364 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 423

Qy    158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
          | ||    || | |||||||  | |||  ||| ||| |  | ||||| ||  | |||||||
Db    424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483

Qy    218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaact 277
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Db    484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543

Qy    278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
          ||||  ||| |||| ||  ||| || |  |||||||| |  || || ||  |||
Db    544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

Qy    338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
          ||||||||  |   | |||||  | |   |     |  |||||||   | |||||| |    |
Db    604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

Qy    398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457
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Db    664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723

Qy    458 acggggccctggaggaggcgcggcgtctgcgggaggggaactgggcatcagtgaggacag 517
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Db    724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

Qy    518 tgctgacgggggccg 532
            |||| | |||||
Db    784 GCATGACTGTGGCCG 798


RESULT   6
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Craig B. B.
;    APPLICANT:  Boise, Lawrence H.
;    TITLE OF INVENTION:  VERTEBRATE APOPTOSIS GENE:
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,670A
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,448
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  ARCD:090--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-470-670A-6
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/798,897
;       FILING DATE:  February 11, 1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Esmond, Robert W.
;       REGISTRATION NUMBER:  32,893
;       REFERENCE/DOCKET NUMBER:  1483.0140001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  579 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  cDNA
US-08-798-897-1


  Query Match             89.7%;  Score 523;  DB 2;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 1e-124;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

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; Sequence 1, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-1


  Query Match             89.7%;  Score 523;  DB 3;  Length 579;
  Best Local Similarity   94.0%;  Pred. No. 1e-124;
  Matches  544;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

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RESULT   2
US-08-978-523-2
; Sequence 2, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540

;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-2


  Query Match             97.4%;  Score 567.8;  DB 3;  Length 579;
  Best Local Similarity   98.8%;  Pred. No. 4.2e-136;
  Matches  572;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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RESULT   3
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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GenCore version 4.5
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	131	22.5	926	3	US-08-470-670A-6	Sequence 6, Appli
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8	123.4	21.2	717	3	US-08-465-485A-20	Sequence 20, Appl
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11	123.4	21.2	5086	3	US-08-465-485A-19	Sequence 19, Appl
12	123.4	21.2	5086	3	US-08-365-486A-14	Sequence 14, Appl
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ALIGNMENTS

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RESULT   1
US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-798-897-2


  Query Match             97.4%;  Score 567.8;  DB 2;  Length 579;
  Best Local Similarity   98.8%;  Pred. No. 4.2e-136;
  Matches  572;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60
```

Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 91 a 173 c 130 g 77 t
ORIGIN

Query Match 19.1%; Score 111.2; DB 46; Length 471;
Best Local Similarity 60.7%; Pred. No. 2.7e-16;
Matches 182; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

```
Qy    134 ccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctgatctgg 193
          || | ||    || || || || |||     ||||| ||| |||  |||| | ||  ||
Db    428 CCCTCCGCCAGGCCGGCGACGACTTCTCCCGCCGCTACCGCCGCGACTTCGCCGAGATGT 369

Qy    194 cggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccaggtctccgacg 253
          |    |||||||| |||| ||   | | || | |  ||||||  ||  |||    || |
Db    368 CCAGCCAGCTGCACCTGACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGG 309

Qy    254 aacttttttcaaggggggccccaactggggccgccttgtagccttctttctctttggggctg 313
          | || ||    |  ||    ||||||||  |  |||| |||||||||   || || |  |
Db    308 AGCTCTTCAGGGACGGGGTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGG 249

Qy    314 cactgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagt 373
            ||||||  ||||| |||||| |||||||   || |||||||   |  |       ||
Db    248 TCATGTGTGTGGAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGT 189

Qy    374 ggatggtggcctacctggagacgcggctggtcgactggatccacagcagtgggggctggg 433
          |||||   |  ||||| |   ||  |||  |  |||||||||    |  || |||||||
Db    188 GGATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGG 129
```

RESULT 15
F08773
LOCUS F08773 299 bp mRNA EST 20-FEB-1995
DEFINITION HSC25B061 normalized infant brain cDNA Homo sapiens cDNA clone c-25b06, mRNA sequence.
ACCESSION F08773
VERSION F08773.1 GI:673075
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
COMMENT On Sep 21, 1992 this sequence version replaced gi:276079.
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-25b06
Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 339.
FEATURES Location/Qualifiers
source 1. .299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-25b06"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
BASE COUNT 67 a 69 c 94 g 67 t 2 others
ORIGIN

Query Match 18.8%; Score 109.6; DB 21; Length 299;
Best Local Similarity 61.2%; Pred. No. 5.5e-16;
Matches 175; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

```
Qy    148 ggagatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcat 207
          || || ||||| ||    || | ||||||  | |||  ||| ||| |  | ||||| ||
Db      1 GGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCAC 60

Qy    208 gtgaccccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggg 267
          | ||||||||  ||||  | ||  ||||    |||||     | ||||| || |  |
Db     61 ATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGAT 120

Qy    268 ggccccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgag 327
          ||    |||||||| ||| |||| ||||| ||   ||| || |  |||||||  |  ||
Db    121 GGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTNCGTGGAA 180

Qy    328 agtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctac 387
          || ||  |||||||||||| |   | ||||| |     |    |  | |||||   | |||
Db    181 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTNGGATCGCAGCTTAGATGGCCACTTAC 240

Qy    388 ctggagacgcggctggtcgactggatccacagcagtgggggctggg 433
          ||| |    |  || |     ||||||||    |  || |||||||
Db    241 CTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 286
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Search completed: July 4, 2000, 01:06:08
Job time: 16527 sec

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Db    301 GATGGGGTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTG 242

Qy    325 gagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcc 384
          ||||| ||||||| ||||||| ||| |||||||   |  |      |||||||   |
Db    241 GAGAGCGTCAACAGGGAGATGTCACCCCTGGTGGACAACATCGCCCTGTGGATGACTGAG 182

Qy    385 tacctggagacgcggctggtcgactggatccacagcagtgggggctggg 433
          |||||| |   ||  |||  |  |||||||||    |  || |||||||
Db    181 TACCTGAACCGGCATCTGCACACCTGGATCCAGGATAACGGAGGCTGGG 133


RESULT  13
W01420
LOCUS       W01420        437 bp    mRNA            EST       18-APR-1996
DEFINITION  za73d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
            BCL-X. ;, mRNA sequence.
ACCESSION   W01420
VERSION     W01420.1  GI:1273428
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785898.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 383.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Homo sapiens"
                     /db_xref="GDB:1243109"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:298187"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT       99 a    106 c    140 g     89 t      3 others
ORIGIN


  Query Match             19.6%;  Score 114.2;  DB 25;  Length 437;
  Best Local Similarity   62.9%;  Pred. No. 5.4e-17;
  Matches  193;  Conservative    0;  Mismatches  113;  Indels    1;  Gaps    1;

Qy    128 accaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctg 187
          | |||||  || |||  || || || ||||| ||    || | ||||||  | |||  ||
Db     16 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 75

Qy    188 atctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccaggtct 247
          | ||| |  | ||||| ||  | ||||||||  ||||  | ||  ||||    |||||
Db     76 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 135

Qy    248 ccgacgaacttttttcaaggggccccaactggggccgccttgtagccttctttctctttg 307
            | ||||| || |  |  ||    |||||||| ||| |||| ||||| ||   ||| |
Db    136 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 195

Qy    308 gggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgc 367
          | |  |||||||| |  || || ||  |||||||||||| |   | ||||| | |   |
Db    196 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 255

Qy    368 aggagtggatggtggcctacctggagacgcggctggtcgac-tggatccacagcagtggg 426
            |  |||||||   | ||||||  |    |  || |  | | ||||||||    |  ||
Db    256 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAAGCCTTGGATCCAGGAGAACGGC 315

Qy    427 ggctggg 433
          |||||||
Db    316 GGCTGGG 322


RESULT  14
AI401297/c
LOCUS       AI401297      471 bp    mRNA            EST       30-MAR-1999
DEFINITION  tg92c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116234 3'
            similar to gb:M13995 PROTEIN BCL-2-BETA (HUMAN);contains TAR1.t2
            MER22 repetitive element ;, mRNA sequence.
ACCESSION   AI401297
VERSION     AI401297.1  GI:4244384
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Apr 7, 1998 this sequence version replaced gi:3035272.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 2629   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 445.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2116234"
                     /clone_lib="NCI_CGAP_CLL1"
                     /tissue_type="B-cell, chronic lymphotic leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
```

```
          determines the means for distribution of the BMAP cDNA clones, this
          record will be updated accordingly when that means is determined.
          Seq primer: M13 Forward
          POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH2.1-apn-b-04-0-UI"
                     /clone_lib="NIH_BMAP_M_S3.1"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S3.1 library is a subtracted library of a
                     series, ultimately derived from a mixture of individually
                     tagged normalized libraries from ten regions of the mouse
                     brain (cerebellum, brain stems, olfactory bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland, striatum, hipoccampus) after a series of
                     subtractions to reduce the representation of cDNAs from
                     which ESTs had already been generated. The following
                     serially subtracted libraries were generated in this
                     process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
                     The subtracted library (NIH_BMAP_M_S3.1) was constructed
                     as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the NIH_BMAP_M_S2 library
                     in the form of single-stranded circles. The remaining
                     single-stranded circles (subtracted library) was purified
                     by hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (LifeTechnologies) to generate the
                     NIH_BMAP_M_S3.1 library. This procedure has been
                     previously described (Bonaldo, Lennon and Soares, Genome
                     Research 6:791-806, 1996)
                     TAG_LIB=NIH_BMAP_M_S3.1
                     TAG_TISSUE=hippocampus
                     TAG_SEQ=TCAAG"
BASE COUNT       86 a    147 c    111 g    110 t
ORIGIN


  Query Match             20.0%;  Score 116.6;  DB 69;  Length 454;
  Best Local Similarity   59.5%;  Pred. No. 1.5e-17;
  Matches  197;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||      |    |   | || | |||||  || | |  || || |||||||| |
Db    331 GGGAGGTGATTCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCAGGCGATGAGTTTG 272

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | ||||| ||  | ||||||||
Db    271 AACTGCGGTACCGGAGAGCGTTCAGTGATCTAACATCCCAGCTTCACATAACCCCAGGGA 212

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggggccccaactggg 280
          | ||  | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    211 CCGCGTATCAGAGCTTTGAGCAGGTAGTGAATGAACTCTTTCGGGATGGAGTAAACTGGG 152

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| | || ||||| ||   |||||| |  |||||||| |  || || ||  ||||||
Db    151 GTCGCATCGTGGCCTTTTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 92

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          |||||  |   | ||||| | |   |       |||||||   |||| ||| |    |  |
Db     91 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTATCTGAATGACCACC 32

Qy    401 tggtcgactggatccacagcagtgggggctg 431
          | |     ||||||||    |  || ||| |
Db     31 TAGAGCCTTGGATCCAGGAGAACGGCGGCCG 1
```

```
RESULT  12
AA939725/c
LOCUS       AA939725      515 bp    mRNA            EST       01-MAY-1998
DEFINITION  vz92a11.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1344668 5' similar to gb:L31532_rna1 Mouse bcl-2 gene
            encoding mbcl-2-beta (MOUSE);, mRNA sequence.
ACCESSION   AA939725
VERSION     AA939725.1  GI:3099269
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2285479.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:693460
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 304.
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1344668"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      125 a    168 c    130 g     92 t
ORIGIN


  Query Match             19.7%;  Score 114.6;  DB 40;  Length 515;
  Best Local Similarity   62.3%;  Pred. No. 4.6e-17;
  Matches  180;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy    145 gctggagatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctg 204
          ||||| ||||| |||       |||| ||| ||   |||| | ||  || |   |||||||
Db    421 GCTGGGGATGACTTCTCTCGTCGCTACCGTCGTGACTTCGCAGAGATGTCCAGTCAGCTG 362

Qy    205 catgtgaccccaggctcagcccagcaacgcttcacccaggtctccgacgaacttttttcaa 264
          ||  |||| ||   | | ||   |  ||||||  ||  |||    || ||||| ||
Db    361 CACCTGACGCCCTTCACCGCGAGGGGACGCTTTGCCACGGTGGTGGAGGAACTCTTCAGG 302

Qy    265 gggggccccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgct 324
          |  ||    ||||||||  |  |||| |||||||||   || || |  |   ||||||
```

(Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_LIB=UI-R-Y0
TAG_TISSUE=Eye
TAG_SEQ=CATTG"
BASE COUNT 88 a 128 c 92 g 96 t
ORIGIN

Query Match 21.6%; Score 125.8; DB 51; Length 404;
Best Local Similarity 61.4%; Pred. No. 1.1e-19;
Matches 202; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy    101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
          ||||||      |    |   |  || | |||||  || | |  ||||| ||||||||
Db    383 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 324

Qy    161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
          |    || | |||| |  | |||  ||||||  |  | ||||| ||| | ||||||||
Db    323 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 264

Qy    221 cagcccagcaacgcttcacccaggtctccgacgaacttttttcaaggggggccccaactggg 280
          ||||  | ||  ||||    |||||     | ||||| ||||  |  ||    |||||||
Db    263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 204

Qy    281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
          | ||| |||| ||||||||   |||||| |  |||||||| |  || || ||  ||||||
Db    203 GTCGCATTGTGGCCTTCTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 144

Qy    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
          ||||| |   | ||||| | |   |       |||||||   |||||||| |    |  |
Db    143 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 84

Qy    401 tggtcgactggatccacagcagtgggggc 429
          | |     ||||||||    |  || |||
Db     83 TAGAGCCTTGGATCCAGGAGAACGGCGGC 55
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RESULT 10
AL134785
LOCUS AL134785 584 bp mRNA EST 29-DEC-1999
DEFINITION DKFZp547K2090_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547K2090 5', mRNA sequence.
ACCESSION AL134785
VERSION AL134785.1 GI:6602972
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 584)
AUTHORS Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT On Jul 7, 1999 this sequence version replaced gi:5866255.
Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES Location/Qualifiers
source 1. .584
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp547K2090"
/clone_lib="547 (synonym: hfbr1)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT 144 a 145 c 173 g 116 t 6 others
ORIGIN

Query Match 20.5%; Score 119.4; DB 79; Length 584;
Best Local Similarity 60.2%; Pred. No. 3.7e-18;
Matches 192; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy     98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
          || |||||      |    |   |  |  | |||||  || |||  || || || ||||
Db    263 CCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGT 322

Qy    158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
          | ||    || | |||||||  | |||  ||| ||| |  | ||||| ||  | |||||||
Db    323 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 382

Qy    218 gctcagcccagcaacgcttcacccaggtctccgacgaacttttcaaggggccccaact 277
          |  ||||  | ||  ||||    |||||     | ||||| || |  |  ||    ||||
Db    383 GGACAGCATATCANAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 442

Qy    278 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
          |||| ||| |||| ||||| ||   ||| || |  |||||||| |  || || ||  |||
Db    443 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 502

Qy    338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
          |||||||| |   | ||||| | |  |  |     |||||||   | ||||||  |    |
Db    503 AGGAGATGCANGTATTGGTGAGTCCNGATCGCACTTGGATGGCCACTTACCTGAATGACC 562

Qy    398 ggctggtcgactggatcca 416
            ||       ||||||||
Db    563 ACCTANANNCTTGGATCCA 581
```

RESULT 11
AW124015/c
LOCUS AW124015 454 bp mRNA EST 22-OCT-1999
DEFINITION UI-M-BH2.1-apn-b-04-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone UI-M-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
ACCESSION AW124015
VERSION AW124015.1 GI:6099545
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 454)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Jul 7, 1999 this sequence version replaced gi:5866278.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH

```
  Query Match             25.5%;  Score 148.8;  DB 109;  Length 549;
  Best Local Similarity   98.7%;  Pred. No. 5.5e-25;
  Matches  150;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    432 ggcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcggga 491
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    261 GGCGGAGTTCACAGCTCTATACGGGGACGGAGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 320

Qy    492 ggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggt 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 380

Qy    552 aactgtaggggccttttttgctagcaagtgaa 583
          |||||||||||||| ||||||||||||||||
Db    381 AACTGTAGGGGCCTTGTTTGCTAGCAAGTGAA 412


RESULT   8
AQ401160
LOCUS       AQ401160      455 bp    DNA              GSS       13-MAR-1999
DEFINITION  HS_5062_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
ACCESSION   AQ401160
VERSION     AQ401160.1  GI:4412503
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 638  row: M  column: 4
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 455.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=638 Col=4 Row=M"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT       80 a    111 c    142 g    117 t      5 others
ORIGIN


  Query Match             23.3%;  Score 135.6;  DB 106;  Length 455;
  Best Local Similarity   92.8%;  Pred. No. 5.9e-22;
  Matches  141;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    432 ggcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcggga 491
          |||||||||||||||||||||||| ||| | |||||||||| ||||||||||||||||
Db    224 GGCGGAGTTCACAGCTCTATACGGTGACAGCGCCCTGGAGGATGCGCGGCGTCTGCGGGA 283

Qy    492 ggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggt 551
          |||||||||||||||||||||||||||||| | |||||||||||| ||||||| ||
Db    284 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACNGTGGCCGTGGCACTTGGGGCCCTTGT 343

Qy    552 aactgtaggggccttttttgctagcaagtgaa 583
          ||||||| |||||||||||  ||||||||||
Db    344 AACTGTANGGGCCTTTTTTGTAGCAAGTGAA 375


RESULT   9
AI716839/c
LOCUS       AI716839      404 bp    mRNA             EST       10-JUN-1999
DEFINITION  UI-R-Y0-acg-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone
            UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
ACCESSION   AI716839
VERSION     AI716839.1  GI:5034095
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On May 18, 1998 this sequence version replaced gi:3136946.
            Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-Y0-acg-g-07-0-UI"
                     /clone_lib="UI-R-Y0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
                     library is a subtracted library derived from an
                     individually-tagged normalized whole-eye (minus the lens)
                     library. The driver for the subtraction consisted of a
                     pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
                      UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
                     3-5 nucleotides present between the Not I site and the
                     oligo-dT track which allows identification of the library
                     of origin of a clone within the mixture. The subtracted
                     library (UI-R-Y0) was constructed as follows: PCR
                     amplified cDNA inserts from previous library clones from
                     which 3' ESTs had  been derived were used as a driver in a
                     hybridization with the normalized  whole-eye library in
                     the form of single-stranded circles. The remaining
                     single-stranded circles (subtracted library) was purified
                     by hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-Y0
                     library. This procedure has been previously described
```

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                    used for subtraction consisted of a pool of 5,000 clones
                    from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                    obtained from non-normalized and normalized mouse brain
                    spinal cord libraries.
                    TAG_LIB=NIH_BMAP_M_S2
                    TAG_TISSUE=corpus-striatum
                    TAG_SEQ=ACGGC"
BASE COUNT      105 a    131 c     85 g    110 t
ORIGIN


  Query Match             26.9%;  Score 156.8;  DB 64;  Length 431;
  Best Local Similarity   90.8%;  Pred. No. 7.1e-27;
  Matches  167;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy     250 gacgaacttttttcaaggggggccccaactggggccgccttgtagccttctttctctttggg 309
           |||||||||||| |||||||||| |||||||||| ||||| || |||||| ||||||||
Db     431 GACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGG 372

Qy     310 gctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcag 369
           ||||| |||||||||||||||||||| || ||||| ||  ||||||||||||||||
Db     371 GCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTGCAG 312

Qy     370 gagtggatggtggcctacctggagacgcggctggtcgactggatccacagcagtgggggc 429
           || |||||||||||||||||||||| || ||||  |||||||||||||||||||||||
Db     311 GATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGGC 252

Qy     430 tggg 433
           ||||
Db     251 TGGG 248


RESULT   6
AQ532175
LOCUS       AQ532175      628 bp    DNA             GSS       18-MAY-1999
DEFINITION  RPCI-11-352L5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-352L5,
            genomic survey sequence.
ACCESSION   AQ532175
VERSION     AQ532175.1  GI:4844050
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 628)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     On Feb 19, 1999 this sequence version replaced gi:4145213.
            Other_GSSs: RPCI-11-352L5.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .628
                     /organism="Homo sapiens"
                     /db_xref="GDB:7635052"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-352L5"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      128 a    130 c    237 g    133 t
ORIGIN


  Query Match             26.1%;  Score 152;  DB 108;  Length 628;
  Best Local Similarity   100.0%;  Pred. No. 1e-25;
  Matches  152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     432 ggcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcggga 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 292

Qy     492 ggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggt 551
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 352

Qy     552 aactgtaggggccttttttgctagcaagtgaa 583
           ||||||||||||||||||||||||||||||||
Db     353 AACTGTAGGGGCCTTTTTTGCTAGCAAGTGAA 384


RESULT   7
AQ665088
LOCUS       AQ665088      549 bp    DNA             GSS       23-JUN-1999
DEFINITION  HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
ACCESSION   AQ665088
VERSION     AQ665088.1  GI:5172856
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 549)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 916  row: B  column: 11
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 549.
FEATURES             Location/Qualifiers
     source          1. .549
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=916 Col=11 Row=B"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      105 a    126 c    190 g    118 t     10 others
ORIGIN
```

```
Qy     61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
          ||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db    214 AAGCTGAGGCAGAAGGGGTATGTTTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 273

Qy    121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 CCGCTACACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 333

Qy    181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
          ||||| |||||||| |||||||||||||||||||| ||||| ||||||||||||||||||
Db    334 TTCTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC 393

Qy    241 caggtctccgacgaacttttttcaaggggcccccaactggg 280
          |||||||| || ||||| || ||||||||||||||||||||
Db    394 CAGGTCTCTGATGAACTCTTCCAAGGGGGCCCCAACTGGG 433
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RESULT 4
AW159063
LOCUS AW159063 416 bp mRNA EST 05-NOV-1999
DEFINITION za50h02.x1 Xenopus EST library Xenopus laevis cDNA clone za50h02 5', mRNA sequence.
ACCESSION AW159063
VERSION AW159063.1 GI:6271092
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 416)
AUTHORS Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,R., Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and McCombie,W.R.
TITLE Expressed sequence tags from Xenopus
JOURNAL Unpublished (1999)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189433.
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.

FEATURES Location/Qualifiers
source 1. .416
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="za50h02"
/clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
/cell_line="W22-TGA"
/dev_stage="tadpole"
/note="Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."

BASE COUNT 108 a 70 c 118 g 120 t
ORIGIN

Query Match 27.5%; Score 160.6; DB 71; Length 416;
Best Local Similarity 72.5%; Pred. No. 9.2e-28;
Matches 208; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```
Qy    296 tctttctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactgg 355
          | ||| | ||||| || ||||||||||||||||||||||||||||||||   || ||
Db      5 TTTTTTTTTTTGGTGCCGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGTCCCCTCTTC 64

Qy    356 tgggacaagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatcc 415
          ||  ||   | || || ||||||||| | || ||||||||    |||   | |||||| |
Db     65 TGCCACGGATTCAAGACTGGATGGTGACATATCTGGAGACAAACCTGAGAGGCTGGATTC 124

Qy    416 acagcagtgggggctgggcggagttcacagctctatacggggacggggccctggaggagg 475
          | |||| ||| |||||  |  ||   | ||||||| ||||| || ||| | || || |
Db    125 AGAGCAATGGATGCTGGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAG 184

Qy    476 cgcggcgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtgg 535
          |  || | |  || |||||||| |||||||| ||| ||| ||  | || || || || |
Db    185 CCAGGAGGCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAACTGGAGCGGTAG 244

Qy    536 cactgggggccctggtaactgtaggggccttttttgctagcaagtga 582
          | ||||| ||  || | || ||||| ||||| ||||| |||||||||
Db    245 CTCTGGGTGCTTTGATGACAGTAGGAGCCTTGTTTGCCAGCAAGTGA 291
```

RESULT 5
AW048567/c
LOCUS AW048567 431 bp mRNA EST 18-SEP-1999
DEFINITION UI-M-BH1-alx-e-10-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alx-e-10-0-UI 3', mRNA sequence.
ACCESSION AW048567
VERSION AW048567.1 GI:5909096
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 431)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Feb 18, 1999 this sequence version replaced gi:4297581.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .431
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-alx-e-10-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver

```
Db    531 AGTGGGGGCT 540


RESULT   2
AA596919
LOCUS       AA596919      362 bp    mRNA            EST       19-SEP-1997
DEFINITION  vo21f08.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
            IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
            sequence.
ACCESSION   AA596919
VERSION     AA596919.1  GI:2412354
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Dec 18, 1996 this sequence version replaced gi:1734345.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:582143
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C3H"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1050567"
                     /clone_lib="Barstead mouse myotubes MPLRB5"
                     /cell_line="C2C12"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [AATTCGGATCCTTG], digested with Not I and cloned into the
                     Not I and Eco RI sites of the modified pT7T3 vector.
                     Library constructed by Bob Barstead. The C2C12 cell line
                     (available from ATCC, catalog # CRL-1772) differentiates
                     rapidly, forming contractile myotubes and producing
                     characteristic muscle proteins. "
BASE COUNT       64 a    116 c    107 g     75 t
ORIGIN


  Query Match             49.4%;  Score 288;  DB 35;  Length 362;
  Best Local Similarity   91.1%;  Pred. No. 2.6e-57;
  Matches  306;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      4 gcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttataag 63
          | ||||||||||||  |||||||||||||||||||| ||||| |||||||||||| ||||||
Db     27 GGGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATAAG 86

Qy     64 ctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgacccg 123
          |||||||||||||||||||||||||||||||||| ||||| |||||||| || ||||||
Db     87 CTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACCCG 146

Qy    124 ctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttc 183
          |||||||||||||||||| || |||||||| ||||| |||||||| ||||| |||||||||
Db    147 CTGCACCAAGCCATGCGTGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTC 206

Qy    184 tctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccag 243
          ||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||||||
Db    207 TCTGAACTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAG 266

Qy    244 gtctccgacgaacttttcaaggggggccccaactggggccgccttgtagccttctttctc 303
          || |||||||||||||| |||||||||| |||||||||| ||||| || |||||| ||
Db    267 GTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTC 326

Qy    304 tttggggctgcactgtgtgctgagagtgtcaacaag 339
          |||||||||| |||||||||||||||||||  |||
Db    327 TTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362


RESULT   3
AW326901
LOCUS       AW326901      433 bp    mRNA            EST       27-JAN-2000
DEFINITION  20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW326901
VERSION     AW326901.1  GI:6762822
KEYWORDS    EST.
SOURCE      Bos taurus.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
            Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1133576.
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 10  row: G  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT       80 a    142 c    143 g     68 t
ORIGIN


  Query Match             44.2%;  Score 257.6;  DB 80;  Length 433;
  Best Local Similarity   95.0%;  Pred. No. 3.1e-50;
  Matches  266;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

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          |||||||||||||||||||||||||||||||||||||||| |||||||||||||| || |||
Db    154 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTAGTGGCAGACTTTGTGGGCTAT 213
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	1	357.2	61.3	540	79	AW258810	AW258810 um74a02.y
	2	288	49.4	362	35	AA596919	AA596919 vo21f08.r
	3	257.6	44.2	433	80	AW326901	AW326901 20104 MAR
	4	160.6	27.5	416	71	AW159063	AW159063 za50h02.x
c	5	156.8	26.9	431	64	AW048567	AW048567 UI-M-BH1-
	6	152	26.1	628	108	AQ532175	AQ532175 RPCI-11-3
	7	148.8	25.5	549	109	AQ665088	AQ665088 HS_5340_B
	8	135.6	23.3	455	106	AQ401160	AQ401160 HS_5062_A
c	9	125.8	21.6	404	51	AI716839	AI716839 UI-R-Y0-a
	10	119.4	20.5	584	79	AL134785	AL134785 DKFZp547K
c	11	116.6	20.0	454	69	AW124015	AW124015 UI-M-BH2.
c	12	114.6	19.7	515	40	AA939725	AA939725 vz92a11.r
	13	114.2	19.6	437	25	W01420	W01420 za73d06.r1
c	14	111.2	19.1	471	46	AI401297	AI401297 tg92c06.x
	15	109.6	18.8	299	21	F08773	F08773 HSC25B061 n
	16	108.8	18.7	472	43	AI180733	AI180733 ub91d09.r
c	17	104.6	17.9	471	34	AA509753	AA509753 vh52c06.r
	18	76.6	13.1	1696	83	AF149300	AF149300 Rattus no
c	19	53.8	9.2	574	81	AW418903	AW418903 ha15d05.x
	20	52.8	9.1	274	20	T29044	T29044 EST66242 Hu
	21	52.6	9.0	516	22	H09884	H09884 ym05b07.r1
c	22	51.8	8.9	714	64	AW072826	AW072826 xa42e07.x
	23	50.2	8.6	640	40	AA981864	AA981864 ua36g07.r
	24	49	8.4	478	61	AI837675	AI837675 UI-M-AK0-
c	25	49	8.4	497	27	AA016399	AA016399 mg88g02.r
	26	49	8.4	540	44	AI326919	AI326919 mj39b01.x
c	27	47.6	8.2	624	44	AI323521	AI323521 mo57b02.x
c	28	47.4	8.1	547	41	AI020744	AI020744 ub01h12.r
c	29	47	8.1	418	34	AA458294	AA458294 vg48c03.r
	30	46.6	8.0	616	44	AI323048	AI323048 mj41h10.y
c	31	46.4	8.0	534	44	AI322704	AI322704 mj39b01.y
c	32	46.4	8.0	545	26	W42014	W42014 mb16g04.r1
	33	46.4	8.0	562	27	AA015184	AA015184 mh33d12.r
	34	45.8	7.9	592	27	AA051441	AA051441 mj41h10.r
	35	45.8	7.9	616	26	W97433	W97433 mf95f12.r1
c	36	45.4	7.8	747	74	AW226585	AW226585 up09f12.x
c	37	45.4	7.8	776	82	CNS010RY	AL099352 Drosophil
c	38	45.4	7.8	925	82	CNS0091P	AL053013 Drosophil
	39	45.2	7.8	925	82	CNS0091P	AL053013 Drosophil
c	40	45.2	7.8	1101	83	CNS0153F	AL104949 Drosophil
c	41	45.2	7.8	1101	83	CNS016R4	AL107098 Drosophil
c	42	44.8	7.7	446	27	AA049970	AA049970 mj39b01.r
c	43	44.8	7.7	1101	83	CNS016MA	AL106924 Drosophil
	44	44.6	7.7	1084	83	CNS0156D	AL105055 Drosophil
c	45	43.8	7.5	997	82	CNS006DN	AL065132 Drosophil

ALIGNMENTS

```
RESULT   1
AW258810
LOCUS       AW258810       540 bp    mRNA            EST       23-DEC-1999
DEFINITION  um74a02.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
            REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
ACCESSION   AW258810
VERSION     AW258810.1  GI:6631791
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137956.
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1009678
            Seq primer: custom primer used
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2300906"
                     /clone_lib="Sugano mouse kidney mkia"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
BASE COUNT       98 a    165 c    170 g    107 t
ORIGIN


  Query Match             61.3%;  Score 357.2;  DB 79;  Length 540;
  Best Local Similarity   90.9%;  Pred. No. 2.7e-73;
  Matches  391;  Conservative    0;  Mismatches   38;  Indels    1;  Gaps    1;

Qy       1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
           |||||||||||||||||  ||||||||||||||||||| ||||| |||||||||||  ||| 
Db     112 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 171

Qy      61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
           |||||||||||||||||||||||||||||||||||||| ||||| |||||||| || |||
Db     172 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 231

Qy     121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
           |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db     232 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 291

Qy     181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
           |||||||| ||||| |||||||| || ||||||||||||||||||||||||||||||||
Db     292 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 351

Qy     241 caggtctccgacgaacttttttcaaggggccccaactggggccgccttgtagccttcttt 300
           ||||| |||||||||||||| |||||||||| |||||||||| ||||| || ||||||
Db     352 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 411

Qy     301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
           ||| |||||||||| ||||||||||||||||||||||| || ||||| ||  |||||||||
Db     412 GTCTATGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 471

Qy     361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
           |||||||| || |||||||||||||||||||||| || ||||  |||||||| ||||||
Db     472 CAAGTGCATGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGAT-CACAGC 530

Qy     421 agtgggggct 430
           ||||||||||
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2000, 20:30:41 ; Search time 795.04 Seconds
(without alignments)
2972.214 Million cell updates/sec

Title: US-09-155-327B-6
Perfect score: 583
Sequence: 1 atggcgaccccagcctcggc.....ctttttttgctagcaagtgaa 583

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
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105: gb_gss12:*
106: gb_gss13:*
107: gb_gss14:*
108: gb_gss15:*
109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

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DR   MGD; MGI:99702; BAX.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; Alternative splicing.
FT   DOMAIN       59     73       BH3.
FT   DOMAIN       98    118       BH1.
FT   DOMAIN      150    165       BH2.
FT   TRANSMEM    172    192       POTENTIAL.
SQ   SEQUENCE   192 AA;  21394 MW;  D2E0B3566579FAFF CRC64;

  Query Match           16.5%;  Score 231;  DB 1;  Length 192;
  Best Local Similarity  27.3%;  Pred. No. 4.44e-25;
  Matches    33;  Conservative   36;  Mismatches  47;  Indels   5;  Gaps   4;

Db     50 PPQDASTKKLSECLRRIGDELDSNM--ELQRMIADVD-T-DSPREVFFRVAADMFADGNF 105
          | : :::  | : :|  |||:::     :  : |::  |  |::: | :|: ::|  |
Qy     33 PGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGP- 91

Db    106 NWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDFLRERLLVWIQDQGGWEGLLSYF 165
          ||||:||:| |:: |   ::   :  |:  :  | : :|  ||: ||:  |||  : : :
Qy     92 NWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALY 151

Db    166 G 166
          |
Qy    152 G 152


Search completed: Fri Jun 23 14:14:55 2000
Job time : 15 secs.
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```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96178771.
RA   Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
RT   "The E1B 19K protein blocks apoptosis by interacting with and
RT   inhibiting the p53-inducible and death-promoting Bax protein.";
RL   Genes Dev. 10:461-477(1996).
RN   [2]
RP   SEQUENCE OF 75-192 FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97147318.
RA   Madison D.L., Pfeiffer S.E.;
RT   "Cloning of the 3' end of rat bax-alpha and corresponding
RT   developmental down-regulation in differentiating primary, cultured
RT   oligodendrocytes.";
RL   Neurosci. Lett. 220:183-186(1996).
RN   [3]
RP   SEQUENCE OF 37-169 FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE; 95129487.
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
CC   -!- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
CC       ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC       HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC       ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC       E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC   -!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
CC       CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC       HIGHEST LEVELS IN THE TESTIS AND OVARY.
CC   -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
CC       THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
CC       APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z26528; CAA81299.1; -.
DR   EMBL; U59184; AAC52998.1; -.
DR   EMBL; U32098; AAA75200.1; -.
DR   EMBL; S76511; AAC60700.1; -.
DR   EMBL; U49729; AAC26327.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; Alternative splicing.
FT   DOMAIN       59     73       BH3.
FT   DOMAIN       98    118       BH1.
FT   DOMAIN      150    165       BH2.
FT   TRANSMEM    172    192       POTENTIAL.
FT   CONFLICT     72     72       S -> N (IN REF. 3).
FT   CONFLICT     76     76       L -> M (IN REF. 2).
FT   CONFLICT    126    126       C -> Y (IN REF. 2).
FT   CONFLICT    149    149       L -> F (IN REF. 3).
FT   CONFLICT    159    159       D -> E (IN REF. 1).
SQ   SEQUENCE   192 AA;  21350 MW;  7B3CD198D56DF589 CRC64;

  Query Match           16.5%;  Score 231;  DB 1;  Length 192;
  Best Local Similarity  27.3%;  Pred. No. 4.44e-25;
  Matches   33;  Conservative   36;  Mismatches  47;  Indels   5;  Gaps   4;

Db     50 PPQDASTKKLSECLRRIGDELDSNM--ELQRMIADVD-T-DSPREVFFRVAADMFADGNF 105
          | : :::  | : :|  |||:::     :  : |::  |  |::: | :|: ::|  |
Qy     33 PGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGP- 91

Db    106 NWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDFLRERLLVWIQDQGGWDGLLSYF 165
          ||||:||:| |:: |   ::   :  |:  :  | : :|  ||: ||:  |||  : : :
Qy     92 NWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALY 151

Db    166 G 166
          |
Qy    152 G 152


RESULT   15
ID   BAXA_MOUSE     STANDARD;      PRT;   192 AA.
AC   Q07813;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN   BAX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X DBA/2;
RX   MEDLINE; 93364978.
RA   Oltvai Z.N., Milliman C.L., Korsmeyer S.J.;
RT   "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT   accelerates programmed cell death.";
RL   Cell 74:609-619(1993).
CC   -!- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
CC       ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC       HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC       ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC       LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC       CESSATION OF SPERM PRODUCTION.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC       E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC   -!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
CC       CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC   -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
CC       THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
CC       APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; L22472; AAA03622.1; -.
DR   HSSP; P53563; 1AF3.
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CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L31532; AAA37282.1; -.
DR   EMBL; M16506; AAA37282.1; JOINED.
DR   EMBL; M16506; AAA37281.1; -.
DR   PIR; A25960; TVMSA1.
DR   PIR; B25960; TVMSB1.
DR   PIR; E37332; E37332.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:88138; BCL2.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   VARSPLIC    193    236       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                GHK -> VGACLVE (IN ISOFORM BCL-2-BETA).
SQ   SEQUENCE   236 AA;  26425 MW;  AA85EF6B0766BE0A CRC64;

  Query Match           41.8%;  Score 584;  DB 1;  Length 236;
  Best Local Similarity  45.2%;  Pred. No. 7.73e-103;
  Matches    75;  Conservative   43;  Mismatches  43;  Indels   5;  Gaps   3;

Db      76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:||  :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
             |||  ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy     148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   13
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ID   AR11_XENLA     STANDARD;      PRT;   204 AA.
AC   Q91828;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR R11 (XR11).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC   Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEAD;
RX   MEDLINE; 95331613.
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X82461; CAA57844.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane.
FT   DOMAIN       101    120       BH1.
FT   DOMAIN       152    167       BH2.
FT   TRANSMEM     181    198       POTENTIAL.
SQ   SEQUENCE   204 AA;  23379 MW;  3BFC6BE6DDA4CA03 CRC64;

  Query Match           39.7%;  Score 554;  DB 1;  Length 204;
  Best Local Similarity  47.4%;  Pred. No. 6.05e-96;
  Matches    72;  Conservative   28;  Mismatches  51;  Indels   1;  Gaps   1;

Db      46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
           | |: :|   : : ||:  | :||| |::|:||||::|||:|  :||| | ||  |||:
Qy      30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db     106 GTNWGRIVAFFSFGRALCVESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
           | ||||:|||| || ||| || ||||  |: :: :||| |||  |  |:: :|||  | :
Qy      90 GPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149

Db     166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
           |||  |  ::|  :|   :     :|||  ||
Qy     150 LYGDGALEEARRLREG-NWASVRTVLTGAVAL 180


RESULT   14
ID   BAXA_RAT       STANDARD;      PRT;   192 AA.
AC   Q63690; Q62995; Q64383;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-FEB-2000 (Rel. 39, Last annotation update)
DE   APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
GN   BAX.
OS   Rattus norvegicus (Rat).
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RL   Blood 79:229-237(1992).
RN   [6]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE; 91066924.
RA   Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.;
RT   "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT   programmed cell death.";
RL   Nature 348:334-336(1990).
RN   [7]
RP   MUTAGENESIS.
RX   MEDLINE; 94239528.
RA   Yin X.-M., Oltvai Z.N., Korsmeyer J.;
RT   "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT   apoptosis and heterodimerization with Bax.";
RL   Nature 369:321-323(1994).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC       II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC       T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC       REGIONS.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M13994; AAA51813.1; ALT_SEQ.
DR   EMBL; M13995; AAA51814.1; ALT_SEQ.
DR   EMBL; M14745; AAA35591.1; -.
DR   EMBL; X06487; CAA29778.1; -.
DR   EMBL; S72602; AAD14111.1; ALT_SEQ.
DR   PIR; A29409; TVHUA1.
DR   PIR; B29409; TVHUB1.
DR   PIR; A24428; TVHUBC.
DR   PIR; C37332; C37332.
DR   PIR; D37332; D37332.
DR   HSSP; P53563; 1AF3.
DR   MIM; 151430; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
KW   Mitochondrion; Chromosomal translocation; Polymorphism;
KW   Disease mutation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       93    107       BH3.
FT   DOMAIN      136    155       BH1.
FT   DOMAIN      187    202       BH2.
FT   TRANSMEM    212    233       POTENTIAL.
FT   VARSPLIC    196    239       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
FT   MUTAGEN     145    145       G->A: NO HETERODIMERIZATION WITH BAX, AND
FT                                LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     188    188       W->A: NO HETERODIMERIZATION WITH BAX, AND
FT                                LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   VARIANT       7      7       T -> S.
FT                                /FTId=VAR_000827.
FT   VARIANT      59     59       P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                MUTATION).
FT                                /FTId=VAR_000828.
FT   VARIANT      93     93       V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                MUTATION).
FT                                /FTId=VAR_000829.
FT   CONFLICT     48     48       I -> F (IN REF. 4).
FT   CONFLICT     59     59       P -> T (IN REF. 3).
FT   CONFLICT    117    117       S -> R (IN REF. 3).
FT   CONFLICT    129    129       R -> C (IN REF. 4).
SQ   SEQUENCE   239 AA;  26266 MW;  3C49F2B714DC9CCB CRC64;

  Query Match           41.9%;  Score 586;  DB 1;  Length 239;
  Best Local Similarity  45.1%;  Pred. No. 2.68e-103;
  Matches   74;  Conservative   44;  Mismatches  41;  Indels   5;  Gaps   3;

Db      81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
           :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy      30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db     141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
           | ||||:|||| ||: :| ||||:|| ||| :  ||  ||: :|  ||: :|||  |
Qy      90 GPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149

Db     201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
           |||  ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy     150 LYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   12
ID   BCL2_MOUSE     STANDARD;      PRT;   236 AA.
AC   P10417; P10418;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=LIVER;
RX   MEDLINE; 87187643.
RA   Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT   "Molecular analysis of mbcl-2: structure and expression of the murine
RT   gene homologous to the human gene involved in follicular lymphoma.";
RL   Cell 49:455-463(1987).
RN   [2]
RP   REVISIONS TO 221-222.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
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RL   Gene 140:291-292(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY;
RX   MEDLINE; 95129487.
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [3]
RP   SEQUENCE OF 19-172 FROM N.A.
RX   MEDLINE; 95059917.
RA   Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA   Lindholm D.;
RT   "bcl-2 messenger RNA is localized in neurons of the developing and
RT   adult rat brain.";
RL   Neuroscience 61:165-177(1994).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH
CC       HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN,
CC       EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULB,
CC       GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI,
CC       CEREBELLAR GRANULE NEURONS, AND IN EPENDYMAL CELLS. IN PRENATAL
CC       BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM
CC       AND IN THE CORTICAL PLATE.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L14680; AAA53662.1; -.
DR   EMBL; U34964; AAA77687.1; -.
DR   EMBL; S74122; CAB33200.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   CONFLICT     42     42       A -> R (IN REF. 2).
FT   CONFLICT    157    157       E -> G (IN REF. 1).
FT   CONFLICT    164    164       S -> Y (IN REF. 2).
FT   CONFLICT    212    212       L -> Q (IN REF. 2).
SQ   SEQUENCE   236 AA;  26622 MW;  E7688CB9071A872A CRC64;

  Query Match           41.9%;  Score 586;  DB 1;  Length 236;
  Best Local Similarity  45.2%;  Pred. No. 2.68e-103;
  Matches   75;  Conservative   43;  Mismatches  43;  Indels   5;  Gaps   3;

Db     76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
          |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy     28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db    136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
          : | ||||:|||| ||: :| ||||:|| ||| :  || ||: :|  ||: :||| |
Qy     88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147

Db    196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
            |||  ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy    148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   11
ID   BCL2_HUMAN     STANDARD;      PRT;   239 AA.
AC   P10415; P10416; Q16197; Q13842;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 86259760.
RA   Tsujimoto Y., Croce C.M.;
RT   "Analysis of the structure, transcripts, and protein products of
RT   bcl-2, the gene involved in human follicular lymphoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN   [2]
RP   REVISIONS TO 96; 110 AND 237.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87002488.
RA   Cleary M.L., Smith S.D., Sklar J.;
RT   "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT   2/immunoglobulin transcript resulting from the t(14;18)
RT   translocation.";
RL   Cell 47:19-28(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 88196071.
RA   Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA   Goldman P., Korsmeyer S.J.;
RT   "Alternative promoters and exons, somatic mutation and deregulation
RT   of the Bcl-2-Ig fusion gene in lymphoma.";
RL   EMBO J. 7:123-131(1988).
RN   [5]
RP   SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA.
RX   MEDLINE; 92096610.
RA   Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT   "Frequent incidence of somatic mutations in translocated BCL2
RT   oncogenes of non-Hodgkin's lymphomas.";
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FT   DOMAIN       129     148       BH1.
FT   DOMAIN       180     195       BH2.
FT   TRANSMEM     210     226       POTENTIAL.
FT   VARSPLIC     126     188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC     189     233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                  FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
FT                                  BCL-X-BETA).
FT   VARSPLIC     194     233       LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
FT                                  -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
FT                                  X(DELTA-TM)).
SQ   SEQUENCE   233 AA;  26132 MW;  24D2AC79887E072E CRC64;

  Query Match           44.0%;  Score 615;  DB 1;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 5.42e-110;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:|||| 
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
            ||:||| |||:|||: ||:::  || :||: :|  ||: :|||  |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    9
ID   BCL2_CHICK     STANDARD;      PRT;   233 AA.
AC   Q00709;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92379084.
RA   Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT   "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT   homologue of the Bcl-2 oncoprotein.";
RL   Biochim. Biophys. Acta 1132:109-113(1992).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND
CC       BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D11382; BAA01978.1; -.
DR   EMBL; D11381; BAA01978.1; JOINED.
DR   EMBL; Z11961; CAA78018.1; -.
DR   PIR; A37332; A37332.
DR   PIR; S24390; S24390.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion.
FT   DOMAIN       10      30       BH4.
FT   DOMAIN       87     101       BH3.
FT   DOMAIN      130     149       BH1.
FT   DOMAIN      181     196       BH2.
FT   TRANSMEM    208     228       POTENTIAL.
FT   CONFLICT     64      64       E -> S (IN REF. 2).
FT   CONFLICT     67      82       GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
FT                                 (IN REF. 2).
FT   CONFLICT    121     121       H -> T (IN REF. 2).
FT   CONFLICT    139     139       G -> V (IN REF. 2).
SQ   SEQUENCE   233 AA;  25687 MW;  5252555ACB6E4C3D CRC64;

  Query Match           42.0%;  Score 587;  DB 1;  Length 233;
  Best Local Similarity  46.6%;  Pred. No. 1.57e-103;
  Matches    76;  Conservative   41;  Mismatches  39;  Indels   7;  Gaps   5;

Db      76 PAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDG 135
           |:||  :| | :| |:| |||||  |::| |:::::|||:|| :|: ||  | :|||: |
Qy      33 PGEG-PAADP-LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90

Db     136 VNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVEL 195
            ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :| :||: :|||  |  |
Qy      91 PNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTAL 150

Db     196 YGN-SM---RPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
           ||: ::   | | : :| |::|:|:  | :|| :|:||::: |
Qy     151 YGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   10
ID   BCL2_RAT       STANDARD;      PRT;   236 AA.
AC   P49950; Q62837; Q64032;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 94193015.
RA   Sato T., Irie S., Krajewski S., Reed J.C.;
RT   "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
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DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
FT                                IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
FT   CONFLICT      6      6       R -> Q (IN REF. 1).
FT   CONFLICT     12     12       F -> S (IN REF. 2).
FT   CONFLICT     64     64       A -> E (IN REF. 2).
FT   CONFLICT     81     81       I -> L (IN REF. 4).
FT   CONFLICT    119    119       A -> V (IN REF. 4).
FT   CONFLICT    143    144       FF -> SS (IN REF. 4).
FT   CONFLICT    199    199       A -> T (IN REF. 4).
FT   CONFLICT    201    201       A -> P (IN REF. 4).
SQ   SEQUENCE   233 AA;  26158 MW;  2B62B6C63864BC8F CRC64;

  Query Match           44.0%;  Score 615;  DB 1;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 5.42e-110;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
            ||:||| |||:|||: ||::: || :||: :|  ||: :|||  |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    8
ID   BCLX_MOUSE     STANDARD;      PRT;   233 AA.
AC   Q64373; Q60657; Q60658; Q61338;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2A4B;
RA   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
RC   STRAIN=C57BL/6; TISSUE=BRAIN;
RX   MEDLINE; 95331139.
RA   Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
RA   Thompson C.B., Nunez G.;
RT   "bcl-XL is the major bcl-x mRNA form expressed during murine
RT   development and its product localizes to mitochondria.";
RL   Development 120:3033-3042(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
RC   TISSUE=PRE-B CELL;
RX   MEDLINE; 95052604.
RA   Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT   "Cloning and molecular characterization of mouse bcl-x in B and T
RT   lymphocytes.";
RL   J. Immunol. 153:4388-4398(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (BETA ISOFORM).
RC   STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97289584.
RA   Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA   Ohta S., Seldin M.F., Nunez G.;
RT   "Genomic organization, promoter region analysis, and chromosome
RT   localization of the mouse bcl-x gene.";
RL   J. Immunol. 158:4750-4757(1997).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY,
CC       WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC   -!- ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-
CC       X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC       BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC       TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC       ACTIVATED.
CC   -!- DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND
CC       POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC       POSTNATAL TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X83574; CAA58557.1; -.
DR   EMBL; L35049; AAA51039.1; -.
DR   EMBL; L35048; AAA51040.1; -.
DR   EMBL; U10102; AAA82174.1; -.
DR   EMBL; U10101; AAA82173.1; -.
DR   EMBL; U10100; AAA82172.1; -.
DR   EMBL; U51279; AAC53460.1; -.
DR   EMBL; U78031; AAB96881.1; -.
DR   EMBL; U78030; AAB96881.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; BCL2L.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
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CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT
CC       ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC       DEVELOPMENT.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z23110; CAA80657.1; -.
DR   EMBL; U26645; AAB07677.1; -.
DR   PIR; A47537; A47537.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; Alternative splicing.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       82     96       BH3.
FT   DOMAIN      125    144       BH1.
FT   DOMAIN      176    191       BH2.
FT   TRANSMEM    206    223       POTENTIAL.
FT   VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                LSRK -> VRTALP (IN SHORT ISOFORM).
SQ   SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;

  Query Match           44.0%;  Score 615;  DB 1;  Length 229;
  Best Local Similarity  52.3%;  Pred. No. 5.42e-110;
  Matches   78;  Conservative   30;  Mismatches  39;  Indels   2;  Gaps   2;

Db      79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
           |  ::||:| ||||||  |:||:||||::|||:|||:| | | || :|||: | ||||:||
Qy      39 ADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVA 98

Db     139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWERFVDLYGNNAAAE 198
           || ||:||| |||:|||  |||::  || :||  :|  ||: :|||  |  |||: |  |
Qy      99 FFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEE 158

Db     199 LRKGQETFNKWLLTGATVAGVLLLGSLLS 227
            |: :|  | |    : ::| : ||:|::
Qy     159 ARRLREG-N-WASVRTVLTGAVALGALVT 185


RESULT    7
ID   BCLX_RAT       STANDARD;      PRT;   233 AA.
AC   P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RC   TISSUE=BRAIN;
RA   Michaelidis T.M.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
RC   TISSUE=THYMUS;
RX   MEDLINE; 96278736.
RA   Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT   "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT   unspliced RNA, promotes apoptosis in promyeloid cells.";
RL   J. Biol. Chem. 271:13258-13265(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY;
RX   MEDLINE; 95129487.
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
CC       THE BETA ISOFORMS PROMOTE APOPTOSIS.
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
CC       BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC       SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC       OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC       DETECTABLE LEVEL OF BCL-X(S).
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82537; CAA57886.1; -.
DR   EMBL; X82537; CAA57887.1; -.
DR   EMBL; U10579; AAA19257.1; -.
DR   EMBL; U72350; AAB17353.1; -.
DR   EMBL; U72349; AAB17352.1; -.
DR   EMBL; U34963; AAA77686.1; -.
DR   EMBL; S76513; AAC60701.1; ALT_INIT.
DR   EMBL; S78284; AAC60702.1; -.
DR   PDB; 1AF3; 07-JUL-97.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
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RX   MEDLINE; 95372373.
RA   Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA   Korsmeyer S.J.;
RT   "Multiple Bcl-2 family members demonstrate selective dimerizations
RT   with Bax.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN   [4]
RP   MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX   MEDLINE; 96170038.
RA   Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA   Korsmeyer S.J.;
RT   "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL   Nature 379:554-556(1996).
RN   [5]
RP   STRUCTURE BY NMR OF 1-209.
RX   MEDLINE; 97172562.
RA   Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA   Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA   Thompson C.B., Fesik S.W.;
RT   "Structure of Bcl-xL-Bak peptide complex: recognition between
RT   regulators of apoptosis.";
RL   Science 275:983-986(1997).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX   MEDLINE; 96256675.
RA   Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA   Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA   Ng S.L., Fesik S.W.;
RT   "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
RT   cell death.";
RL   Nature 381:335-341(1996).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC       ISOFORM PROMOTES APOPTOSIS.
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCX-X(L) (SHOWN HERE),
CC       BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC       THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC       LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC       LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z23116; CAA80662.1; -.
DR   EMBL; Z23115; CAA80661.1; -.
DR   EMBL; U72398; AAB17354.1; -.
DR   PDB; 1BXL; 29-OCT-97.
DR   PDB; 1LXL; 21-APR-97.
DR   PDB; 1MAZ; 21-APR-97.
DR   MIM; 600039; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
FT                                VGDVDS (IN ISOFORM BCL-X(BETA)).
FT   MUTAGEN     131    133       FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     135    137       VNW->AIL: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN     138    140       GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN     138    138       G->A: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     148    148       G->E: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     188    189       WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT                                BY ABOUT HALF.
FT   CONFLICT     70     70       G -> A (IN CAA80661).
SQ   SEQUENCE   233 AA;  26049 MW;  E09D3CDD851AE9BE CRC64;

  Query Match           44.1%;  Score 616;  DB 1;  Length 233;
  Best Local Similarity 53.1%;  Pred. No. 3.18e-110;
  Matches   77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||:::  || :||: :|  ||: :||| | |||: |  |:|
Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | |      ::| | ||:|
Qy    161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    6
ID   BCLX_CHICK     STANDARD;      PRT;   229 AA.
AC   Q07816; Q98908;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BCLX OR BCL-X.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A. (SHORT FORM).
RX   MEDLINE; 93364977.
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG FORM).
RC   STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=TESTIS;
RX   MEDLINE; 97264485.
RA   Vilagrasa X., Mezquita C., Mezquita J.;
RT   "Differential expression of bcl-2 and bcl-x during chicken
RT   spermatogenesis.";
RL   Mol. Reprod. Dev. 47:26-29(1997).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC       ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
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CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       POTENTIAL.
SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;

  Query Match           66.6%;  Score 931;  DB 1;  Length 228;
  Best Local Similarity  67.9%;  Pred. No. 3.73e-184;
  Matches   125;  Conservative   35;  Mismatches  21;  Indels   3;  Gaps   2;

Db      48 SRALVEDLVRYKLCQRSLV--PEPS-GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
           :|||| |:| ||| |:: |  : |: |:|: :|| |||||||||| |||::||::::|:|
Qy      10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69

Db     105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
           ||||:|  ||::|:  ||||| ||||:||||:|||||||||||||| ||: ::|:|||:|
Qy      70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAY 129

Db     165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
           ||| | |||:|:||| | :|||||:||||| |||||||::||||||||||||:||||:
Qy     130 LETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189

Db     225 FASK 228
           ||||
Qy     190 FASK 193


RESULT    4
ID   BCLX_PIG       STANDARD;      PRT;   233 AA.
AC   O77737;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
CC       THE BETA ISOFORMS PROMOTE APOPTOSIS.
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001203; CAA04597.1; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;

  Query Match           44.2%;  Score 618;  DB 1;  Length 233;
  Best Local Similarity  53.8%;  Pred. No. 1.10e-110;
  Matches    78;  Conservative   29;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||:::  || :||: :|  ||: :||| |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTLAGVVLLGSL 229
           : :|  | |       |:| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    5
ID   BCLX_HUMAN     STANDARD;      PRT;   233 AA.
AC   Q07817; Q92976;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RX   MEDLINE; 93364977.
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (BETA ISOFORM).
RA   Inohara N., Ohta S.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
```

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CC   ---------------------------------------------------------------------
DR   EMBL; U59747; AAB09055.1; -.
DR   EMBL; D87461; BAA19666.1; -.
DR   HSSP; P53563; 1AF3.
DR   MIM; 601931; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;

  Query Match           99.0%;  Score 1383;  DB 1;  Length 193;
  Best Local Similarity  99.0%;  Pred. No. 2.09e-292;
  Matches   191;  Conservative    1;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193


RESULT    2
ID   BCLW_MOUSE     STANDARD;      PRT;   193 AA.
AC   P70345;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-W.
GN   BCL2L2 OR BCLW.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96358615.
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/10J;
RX   MEDLINE; 98160183.
RA   Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA   Russell L.D., Macgregor G.R.;
RT   "Testicular degeneration in Bclw-deficient mice.";
RL   Nat. Genet. 18:251-256(1998).
CC   -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC       IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC       AND SALIVARY GLAND.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59746; AAB09056.1; -.
DR   EMBL; AF030769; AAB86430.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:108052; BCL2L2.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;

  Query Match           98.8%;  Score 1380;  DB 1;  Length 193;
  Best Local Similarity  97.9%;  Pred. No. 1.10e-291;
  Matches   189;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193


RESULT    3
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR R1 (XR1) (FRAGMENT).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC   Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEAD;
RX   MEDLINE; 95331613.
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:14:40 2000; MasPar time 7.84 Seconds
749.617 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 46.104; Variance 80.361; scale 0.574

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1383	99.0	193	1	BCLW_HUMAN	APOPTOSIS REGULATOR BC	2.09e-292
2	1380	98.8	193	1	BCLW_MOUSE	APOPTOSIS REGULATOR BC	1.10e-291
3	931	66.6	228	1	AR1_XENLA	APOPTOSIS REGULATOR R1	3.73e-184
4	618	44.2	233	1	BCLX_PIG	APOPTOSIS REGULATOR BC	1.10e-110
5	616	44.1	233	1	BCLX_HUMAN	APOPTOSIS REGULATOR BC	3.18e-110
6	615	44.0	229	1	BCLX_CHICK	APOPTOSIS REGULATOR BC	5.42e-110
7	615	44.0	233	1	BCLX_RAT	APOPTOSIS REGULATOR BC	5.42e-110
8	615	44.0	233	1	BCLX_MOUSE	APOPTOSIS REGULATOR BC	5.42e-110
9	587	42.0	233	1	BCL2_CHICK	APOPTOSIS REGULATOR BC	1.57e-103
10	586	41.9	236	1	BCL2_RAT	APOPTOSIS REGULATOR BC	2.68e-103
11	586	41.9	239	1	BCL2_HUMAN	APOPTOSIS REGULATOR BC	2.68e-103
12	584	41.8	236	1	BCL2_MOUSE	APOPTOSIS REGULATOR BC	7.73e-103
13	554	39.7	204	1	AR11_XENLA	APOPTOSIS REGULATOR R1	6.05e-96
14	231	16.5	192	1	BAXA_RAT	APOPTOSIS REGULATOR BA	4.44e-25
15	231	16.5	192	1	BAXA_MOUSE	APOPTOSIS REGULATOR BA	4.44e-25
16	229	16.4	192	1	BAXA_BOVIN	APOPTOSIS REGULATOR BA	1.12e-24
17	228	16.3	143	1	BAXD_HUMAN	BAX PROTEIN, CYTOPLASM	1.78e-24
18	228	16.3	192	1	BAXA_HUMAN	APOPTOSIS REGULATOR BA	1.78e-24
19	226	16.2	211	1	BAK_HUMAN	BCL-2 HOMOLOGOUS ANTAG	4.50e-24
20	225	16.1	211	1	BAK2_HUMAN	BCL-2 HOMOLOGOUS ANTAG	7.14e-24
21	218	15.6	218	1	BAXB_HUMAN	APOPTOSIS REGULATOR BA	1.79e-22
22	210	15.0	208	1	BAK_MOUSE	BCL-2 HOMOLOGOUS ANTAG	6.86e-21
23	183	13.1	177	1	NR13_COTJA	APOPTOSIS REGULATOR NR	1.15e-15
24	156	11.2	271	1	CED9_CAEBR	APOPTOSIS REGULATOR CE	1.11e-10
25	155	11.1	172	1	BFL1_MOUSE	BCL2-RELATED PROTEIN A	1.68e-10
26	149	10.7	175	1	BFL1_HUMAN	BCL2-RELATED PROTEIN A	1.95e-09
27	150	10.7	350	1	MCL1_HUMAN	INDUCED MYELOID LEUKEM	1.30e-09
28	148	10.6	280	1	CED9_CAEEL	APOPTOSIS REGULATOR CE	2.93e-09
29	131	9.4	179	1	EAR_ASFE4	APOPTOSIS REGULATOR BC	2.38e-06
30	130	9.3	179	1	EAR_ASFM2	APOPTOSIS REGULATOR BC	3.49e-06
31	130	9.3	179	1	EAR_ASFB7	APOPTOSIS REGULATOR BC	3.49e-06
32	98	7.0	680	1	NOLO_RHISN	NODULATION PROTEIN NOL	2.93e-01
33	95	6.8	585	1	YH70_SYNY3	HYPOTHETICAL 67.1 KD P	7.61e-01
34	93	6.7	372	1	LIGC_TRAVE	LIGNINASE C PRECURSOR	1.42e+00
35	94	6.7	421	1	EXG_YARLI	GLUCAN 1,3-BETA-GLUCOS	1.04e+00
36	93	6.7	459	1	DINF_ECOLI	DNA-DAMAGE-INDUCIBLE P	1.42e+00
37	94	6.7	522	1	GAG_HV2G1	GAG POLYPROTEIN [CONTA	1.04e+00
38	94	6.7	569	1	Y4FN_RHISN	PROBABLE ABC TRANSPORT	1.04e+00
39	94	6.7	4543	1	LRP1_CHICK	LOW-DENSITY LIPOPROTEI	1.04e+00
40	92	6.6	321	1	YHZ8_YEAST	HYPOTHETICAL 36.5 KD P	1.93e+00
41	92	6.6	500	1	ARAA_SALTY	L-ARABINOSE ISOMERASE	1.93e+00
42	92	6.6	521	1	MEFD_HUMAN	MYOCYTE-SPECIFIC ENHAN	1.93e+00
43	92	6.6	691	1	COMA_NEIGO	COMPETENCE PROTEIN COM	1.93e+00
44	92	6.6	843	1	PULA_THEMA	PULLULANASE PRECURSOR	1.93e+00
45	92	6.6	906	1	HELY_MYCTU	PUTATIVE HELICASE HELY	1.93e+00

ALIGNMENTS

```
RESULT    1
ID   BCLW_HUMAN     STANDARD;      PRT;   193 AA.
AC   Q92843;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-W (KIAA0271).
GN   BCL2L2 OR BCLW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96358615.
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97191544.
RA   Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. VI.
RT   The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT   analysis of cDNA clones from cell line KG-1 and brain.";
RL   DNA Res. 3:321-329(1996).
CC   -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC       IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC       AND SALIVARY GLAND.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
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```
PT   especially by rescuing cells from apoptosis
PS   Claim 2; Pages 25-26; 30pp; English.
CC   The present sequence represents "Deprenyl" (RTM)-induced protein (DIP),
CC   a novel protein in neural cells. This protein is induced by the
CC   neuroactive drug "Deprenyl" (RTM). DIP 1 and compounds which modulate
CC   its activity can be used for the diagnosis and treatment of neuro-
CC   degenerative disorders, particularly apoptosis in neural cells. Such
CC   apoptosis is associated with diseases such as Alzheimer's, Parkinson's
CC   and Huntington's, as well as cerebellar degeneration and oligodendrocyte
CC   death in multiple sclerosis.
SQ   Sequence   225 AA;

  Query Match           44.9%;  Score 623;  DB 1;  Length 225;
  Best Local Similarity  52.4%;  Pred. No. 1.06e-47;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     77 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 136
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    137 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 196
          ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: | ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    197 KGQERFNRWFLTGMTVAGVVLLGSL 221
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   15
ID   W31530 standard; Protein; 233 AA.
AC   W31530;
DT   19-FEB-1998  (first entry)
DE   Human anti-apoptotic BCL-XL protein.
KW   BCL-XL; anti-apoptotic protein; human; nuclear factor-kappa B;
KW   NF-kappa B; inhibitor; organ transplant; tissue transplant;
KW   inflammation; gene therapy; endothelial cell.
OS   Homo sapiens.
PN   WO9730083-A1.
PD   21-AUG-1997.
PF   13-FEB-1997; E00676.
PR   19-APR-1996; US-634995.
PR   14-FEB-1996; US-601515.
PA   (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
PA   (NOVS ) NOVARTIS AG.
PI   Bach FH,  Ferran C;
DR   WPI; 97-424975/39.
PT   Recombinant endothelial cell containing DNA encoding anti-apoptotic
PT   protein  - is less susceptible to inflammatory response and is
PT   useful for generating tissues or organs for transplantation
PS   Claim 6; Page 46; 75pp; English.
CC   This protein sequence comprises human BCL-XL, a protein capable of
CC   blocking or suppressing NF-kappa B (NF-kB) activation.  A claimed
CC   method of genetically modifying a mammalian endothelial cell to
CC   render it less susceptible to an inflammatory or other
CC   immunological stimulus comprises inserting into the cell, DNA
CC   encoding an anti-apoptotic protein able to inhibit NF-kB, and
CC   expressing the cell such that NF-kB activation of the cell is
CC   inhibited in the presence of the the cellular activating stimulus.
CC   Suitable anti-apoptotic proteins include A20 (see W31528), BCL-2
CC   (see W31529), BCL-XL and A1 (see W31531) and their deletion mutants
CC   capable of inhibiting NF-kB, such as polypeptides comprising amino
CC   acid residues 5-24, 86-100, 129-148 and 180-195 of BCL-XL.  Also
CC   claimed are: (1) a mammalian endothelial cell modified by the above
CC   method: and (2) a non-human transgenic or somatic recombinant
CC   mammal comprising DNA encoding an anti-apoptotic protein of a
CC   different species.  The method can be used to generate donor
CC   endothelial cells or graftable tissues or organs for
CC   transplantation into recipient species.
SQ   Sequence   233 AA;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 1.06e-47;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
          ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: | ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


Search completed: Fri Jun 23 14:17:53 2000
Job time : 12 secs.
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CC   viable in culture for an extended period. In contrast, if they act as
CC   cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC   conditions associated with prolonged cell life span such as cancer
CC   (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC   diseases. They may also be used to cause cell death in, and hence
CC   control, parasites.
SQ   Sequence   192 AA;

  Query Match           95.7%;  Score 1326;  DB 1;  Length 192;
  Best Local Similarity  94.3%;  Pred. No. 7.33e-117;
  Matches   181;  Conservative    8;  Mismatches   2;  Indels   1;  Gaps   1;

Db      1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          :||||:|||||| |||||:||||||||||||||||||||||||||||||||||||||||||
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db    121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||:|:|||||||||||||||:||||||||||:|||||||||| | ||:|||||||
Qy    122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    181 ALVTVGAFFASK 192


RESULT   12
ID   W36048 standard; Protein; 168 AA.
AC   W36048;
DT   22-APR-1998  (first entry)
DE   Mouse bcl-w protein.
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease.
OS   Mus sp.
PN   WO9735971-A1.
PD   02-OCT-1997.
PF   27-MAR-1997; AU0199.
PR   27-MAR-1996; AU-008965.
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
PI   Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR   WPI; 97-489635/45.
DR   N-PSDB; T96578.
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
PS   Claim 6; Page 50-51; 86pp; English.
CC   This sequence represents a novel protein, bcl-w, encoded by the mouse
CC   bcl-2 gene family. This gene promotes cell survival, so its modulation
CC   is useful in treatment of cancer or auto-immune diseases, degenerative
CC   diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC   degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC   or in cell transplants. Up-regulation of the gene can also be used to
CC   modify cell lines cultured in vivo, e.g. to develop new lines, to
CC   facilitate isolation of hybridomas and to increase survival of primary
CC   explants during genetic modification. It can be used to produce
CC   recombinant Bcl-w for therapy, diagnosis, antibody production or
CC   screening of potential modulators.
SQ   Sequence   168 AA;

  Query Match           89.1%;  Score 1235;  DB 1;  Length 168;
  Best Local Similarity 100.0%;  Pred. No. 7.82e-108;
  Matches   168;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168


RESULT   13
ID   W59884 standard; Protein; 365 AA.
AC   W59884;
DT   20-NOV-1998  (first entry)
DE   Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent.
OS   Homo sapiens.
PN   WO9831800-A2.
PD   23-JUL-1998.
PF   21-JAN-1998; U00960.
PR   21-JAN-1997; US-034205.
PR   21-JAN-1997; US-034204.
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
PI   Su JY;
DR   WPI; 98-414099/35.
DR   N-PSDB; V41925.
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
PS   Claim 1; Fig 12A-12D; 120pp; English.
CC   This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
SQ   Sequence   365 AA;

  Query Match           75.1%;  Score 1041;  DB 1;  Length 365;
  Best Local Similarity  96.5%;  Pred. No. 1.22e-88;
  Matches   139;  Conservative    5;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          |:||||:|||||||||||||:||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGW 144
          |||:|:||||||||||||||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGW 144


RESULT   14
ID   W19396 standard; protein; 225 AA.
AC   W19396;
DT   05-MAR-1998  (first entry)
DE   "Deprenyl" (RTM)-induced protein 1.
KW   Deprenyl-induced protein; neuroactive drug; neural cell; apoptosis;
KW   neurodegenerative disorder; oligodendrocyte; multiple sclerosis.
OS   Rattus rattus.
PN   WO9725421-A2.
PD   17-JUL-1997.
PF   21-DEC-1996; E05800.
PR   12-JAN-1996; GB-000660.
PA   (NOVS ) NOVARTIS AG.
PI   Furst P,  Tatton WG,  Waldmeier P;
DR   WPI; 97-384980/35.
PT   New isolated "Deprenyl" (RTM)-induced protein - used to develop
PT   products for use in the diagnosis and treatment of neural disorders,
```

KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
OS Homo sapiens.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR N-PSDB; X25134.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 37; 52pp; English.
CC The present sequence is described of a derivative of human Bcl-w
CC (see also Y05530), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
SQ Sequence 193 AA;

Query Match 96.0%; Score 1331; DB 1; Length 193;
Best Local Similarity 93.8%; Pred. No. 2.34e-117;
Matches 181; Conservative 9; Mismatches 2; Indels 1; Gaps 1;

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Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||:|||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|:|||||||| |||||||||:|||||||||||:|||||||||| | ||:|||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     180 GALVTVGAFFASK 192
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RESULT 10
ID W36047 standard; Protein; 193 AA.
AC W36047;
DT 22-APR-1998 (first entry)
DE Human bcl-w protein.
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
OS Homo sapiens.
PN WO9735971-A1.
PD 02-OCT-1997.
PF 27-MAR-1997; AU0199.
PR 27-MAR-1996; AU-008965.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
DR WPI; 97-489635/45.
DR N-PSDB; T96577.
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
PS Claim 6; Page 48; 86pp; English.
CC This sequence represents a novel human protein, bcl-w, encoded by the
CC bcl-2 gene family and extracted from an adult brain library. This gene
CC promotes cell survival, so its modulation is useful in treatment of
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.
SQ Sequence 193 AA;

Query Match 96.0%; Score 1331; DB 1; Length 193;
Best Local Similarity 93.8%; Pred. No. 2.34e-117;
Matches 181; Conservative 9; Mismatches 2; Indels 1; Gaps 1;

```
Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||:|||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|:|||||||| |||||||||:|||||||||||:|||||||||| | ||:|||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     180 GALVTVGAFFASK 192
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RESULT 11
ID W97394 standard; Protein; 192 AA.
AC W97394;
DT 20-MAY-1999 (first entry)
DE Mammalian bcl-y protein.
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
OS Mammalia.
PN US5883229-A.
PD 16-MAR-1999.
PF 25-NOV-1997; 978523.
PR 23-FEB-1996; US-012201.
PR 11-FEB-1997; US-798897.
PR 25-NOV-1997; US-978523.
PA (COCE-) COCENSYS INC.
PI Guastella J;
DR WPI; 99-214150/18.
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
PS Claim 2; Columns 19-22; 26pp; English.
CC The present sequence represents a mammalian bcy-1 protein.
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain

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SQ   Sequence   193 AA;

  Query Match           96.5%;  Score 1337;  DB 1;  Length 193;
  Best Local Similarity  94.3%;  Pred. No. 5.93e-118;
  Matches   182;  Conservative    8;  Mismatches   2;  Indels   1;  Gaps   1;

Db      1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          |:||||:|||||||| |||||:||||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|:|||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    180 GALVTVGAFFASK 192


RESULT    7
ID   W61392 standard; Protein; 193 AA.
AC   W61392;
DT   02-OCT-1998  (first entry)
DE   Human bcl-y protein.
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
OS   Homo sapiens.
PN   US5789201-A.
PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   N-PSDB; V28334.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Example; Column 17/18; 27pp; English.
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway.  The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity.  bcl-y falls in the apoptosis
CC   activity category.  The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo.  Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
SQ   Sequence   193 AA;

  Query Match           96.5%;  Score 1337;  DB 1;  Length 193;
  Best Local Similarity  94.3%;  Pred. No. 5.93e-118;
  Matches   182;  Conservative    8;  Mismatches   2;  Indels   1;  Gaps   1;

Db      1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          |:||||:|||||||| |||||:||||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|:|||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    180 GALVTVGAFFASK 192


RESULT    8
ID   W97393 standard; Protein; 192 AA.
AC   W97393;
DT   20-MAY-1999  (first entry)
DE   Protein sequence of the specification.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
OS   Unidentified.
PN   US5883229-A.
PD   16-MAR-1999.
PF   25-NOV-1997; 978523.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PR   25-NOV-1997; US-978523.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 99-214150/18.
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
PS   Disclosure; Columns 19-20; 26pp; English.
CC   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC   protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC   thought to be involved in programmed cell death (apoptosis and necrosis).
CC   Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC   with a disruption of the cell death pathway. If they act as cell death
CC   inhibitors, they may be used in therapies to treat subjects suffering
CC   from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC   degenerative diseases (especially multiple sclerosis), myocardial
CC   infarction, vitally induced cell death, aging, spinal cord injuries and
CC   amyotrophic lateral sclerosis- conditions where cells under go premature
CC   cell death as a result of triggers which may or may not be apparent.
CC   They may also be used in this way to develop cell lines which remain
CC   viable in culture for an extended period. In contrast, if they act as
CC   cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC   conditions associated with prolonged cell life span such as cancer
CC   (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC   diseases. They may also be used to cause cell death in, and hence
CC   control, parasites.
SQ   Sequence   192 AA;

  Query Match           96.1%;  Score 1332;  DB 1;  Length 192;
  Best Local Similarity  95.3%;  Pred. No. 1.86e-117;
  Matches   183;  Conservative    7;  Mismatches   1;  Indels   1;  Gaps   1;

Db      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          :||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db    121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||||:|:||||||||||||||:|||||||||||:|||||||||| | ||:|||||||
Qy    122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    181 ALVTVGAFFASK 192


RESULT    9
ID   Y05532 standard; Protein; 193 AA.
AC   Y05532;
DT   05-JUL-1999  (first entry)
DE   Human Bcl-w protein essential for spermatogenesis.
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PD   04-AUG-1998.
PF   11-FEB-1997; 798897.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 98-446079/38.
DR   N-PSDB; V283333.
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
PS   Example; Fig 3A; 27pp; English.
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway.  The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity.  bcl-y falls in the apoptosis
CC   activity category.  The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo.  Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
SQ   Sequence   193 AA;

  Query Match           96.9%;  Score 1343;  DB 1;  Length 193;
  Best Local Similarity  95.3%;  Pred. No. 1.50e-118;
  Matches   184;  Conservative    7;  Mismatches   1;  Indels   1;  Gaps   1;

Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||:|:||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     180 GALVTVGAFFASK 192


RESULT    5
ID   Y05530 standard; Protein; 193 AA.
AC   Y05530;
DT   05-JUL-1999  (first entry)
DE   Human Bcl-w protein essential for spermatogenesis.
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
OS   Homo sapiens.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   N-PSDB; X25132.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Claim 2; Page 33; 52pp; English.
CC   The present sequence is human Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see X25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   193 AA;

  Query Match           96.8%;  Score 1341;  DB 1;  Length 193;
  Best Local Similarity  94.8%;  Pred. No. 2.38e-118;
  Matches   183;  Conservative    8;  Mismatches   1;  Indels   1;  Gaps   1;

Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||:|||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|:|||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     180 GALVTVGAFFASK 192


RESULT    6
ID   W97392 standard; Protein; 193 AA.
AC   W97392;
DT   20-MAY-1999  (first entry)
DE   The human bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
OS   Homo sapiens.
PN   US5883229-A.
PD   16-MAR-1999.
PF   25-NOV-1997; 978523.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PR   25-NOV-1997; US-978523.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 99-214150/18.
DR   N-PSDB; X15946.
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
PS   Claim 1; Columns 17-18; 26pp; English.
CC   The present sequence represents human bcl-y protein (Hbcl-y). The
CC   specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAVALG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAVALG 180

Db     181 ALVTVGAFFASK 192
           ||||||||||||
Qy     181 ALVTVGAFFASK 192


RESULT    2
ID   Y05531 standard; Protein; 193 AA.
AC   Y05531;
DT   05-JUL-1999  (first entry)
DE   Mouse Bcl-w protein essential for spermatogenesis.
KW   Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW   animal model.
OS   Mus sp.
PN   WO9913710-A1.
PD   25-MAR-1999.
PF   16-SEP-1998; AU0764.
PR   16-SEP-1997; AU-009228.
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR   WPI; 99-243890/20.
DR   N-PSDB; X25133.
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
PS   Claim 2; Page 35; 52pp; English.
CC   The present sequence is mouse Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see X25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
SQ   Sequence   193 AA;

  Query Match           97.0%;  Score 1345;  DB 1;  Length 193;
  Best Local Similarity  95.9%;  Pred. No. 9.52e-119;
  Matches   185;  Conservative    6;  Mismatches   1;  Indels   1;  Gaps   1;

Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||:|||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           ||||||||||||
Qy     180 GALVTVGAFFASK 192


RESULT    3
ID   W97391 standard; Protein; 193 AA.
AC   W97391;
DT   20-MAY-1999  (first entry)
DE   The rat bcl-y protein.
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
OS   Rattus sp.
PN   US5883229-A.
PD   16-MAR-1999.
PF   25-NOV-1997; 978523.
PR   23-FEB-1996; US-012201.
PR   11-FEB-1997; US-798897.
PR   25-NOV-1997; US-978523.
PA   (COCE-) COCENSYS INC.
PI   Guastella J;
DR   WPI; 99-214150/18.
DR   N-PSDB; X15945.
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
PS   Disclosure; Columns 15-18; 26pp; English.
CC   The present sequence represents rat bcl-y protein (Rbcl-y). The
CC   specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
SQ   Sequence   193 AA;

  Query Match           96.9%;  Score 1343;  DB 1;  Length 193;
  Best Local Similarity  95.3%;  Pred. No. 1.50e-118;
  Matches   184;  Conservative    7;  Mismatches   1;  Indels   1;  Gaps   1;

Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |:||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Qy       1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db     121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||:|:|||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy     121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db     181 GALVTVGAFFASK 193
           ||||||||||||
Qy     180 GALVTVGAFFASK 192


RESULT    4
ID   W61391 standard; Protein; 193 AA.
AC   W61391;
DT   02-OCT-1998  (first entry)
DE   Rat bcl-y protein.
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
OS   Rattus sp.
PN   US5789201-A.
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:17:41 2000; MasPar time 7.56 Seconds
601.720 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFVGY.....VTGAVALGALVTVGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 32.566; Variance 139.419; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1386	100.0	192	1	Y05533	Mouse Bcl-w protein de	8.04e-123
2	1345	97.0	193	1	Y05531	Mouse Bcl-w protein es	9.52e-119
3	1343	96.9	193	1	W97391	The rat bcl-y protein.	1.50e-118
4	1343	96.9	193	1	W61391	Rat bcl-y protein.	1.50e-118
5	1341	96.8	193	1	Y05530	Human Bcl-w protein es	2.38e-118
6	1337	96.5	193	1	W97392	The human bcl-y protei	5.93e-118
7	1337	96.5	193	1	W61392	Human bcl-y protein.	5.93e-118
8	1332	96.1	192	1	W97393	Protein sequence of th	1.86e-117
9	1331	96.0	193	1	Y05532	Human Bcl-w protein es	2.34e-117
10	1331	96.0	193	1	W36047	Human bcl-w protein.	2.34e-117
11	1326	95.7	192	1	W97394	Mammalian bcl-y protei	7.33e-117
12	1235	89.1	168	1	W36048	Mouse bcl-w protein.	7.82e-108
13	1041	75.1	365	1	W59884	Amino acid sequence of	1.22e-88
14	623	44.9	225	1	W19396	"Deprenyl" (RTM)-induc	1.06e-47
15	623	44.9	233	1	W31530	Human anti-apoptotic B	1.06e-47
16	623	44.9	233	1	R68887	Human thymus BCL-XL.	1.06e-47
17	623	44.9	233	1	W05821	Bcl-XL protein.	1.06e-47
18	556	40.1	239	1	W87810	A human Bcl-2 protein.	3.14e-41
19	545	39.3	239	1	W87812	A human Bcl-2-alpha pr	3.60e-40
20	545	39.3	239	1	R71404	Human bcl-2 alpha prot	3.60e-40
21	545	39.3	239	1	R70331	Human bcl-2 protein.	3.60e-40
22	545	39.3	239	1	R42312	Bcl-2 oncogene product	3.60e-40
23	545	39.3	239	1	W40217	Human bcl-2.	3.60e-40
24	545	39.3	239	1	P80987	Sequence of bcl-2-alph	3.60e-40
25	545	39.3	239	1	R47344	Human oncogene bcl-2 p	3.60e-40
26	542	39.1	232	1	W01019	Apoptosis-blocking pro	6.99e-40
27	542	39.1	232	1	W94346	Human Bcl-2 mutant pro	6.99e-40
28	542	39.1	236	1	W87811	A murine Bcl-2 protein	6.99e-40
29	542	39.1	239	1	W94345	Human Bcl-2 wild-type	6.99e-40
30	542	39.1	239	1	W01018	Apoptosis-blocking pro	6.99e-40
31	535	38.6	190	1	R68884	Chicken lymphoid BCL-X	3.29e-39
32	535	38.6	232	1	W94347	Human Bcl-2 mutant pro	3.29e-39
33	535	38.6	232	1	W01020	Apoptosis-blocking pro	3.29e-39
34	533	38.5	235	1	W48312	Mouse BCL-x gamma.	5.13e-39
35	531	38.3	239	1	W02383	Human BCL2.	7.98e-39
36	491	35.4	205	1	R68886	Human thymus BCL-2.	5.46e-35
37	491	35.4	205	1	W31529	Human anti-apoptotic B	5.46e-35
38	491	35.4	205	1	W87813	A human Bcl-2-beta pro	5.46e-35
39	491	35.4	205	1	R71405	Human bcl-2 beta prote	5.46e-35
40	491	35.4	205	1	R70332	Human bcl-2 protein.	5.46e-35
41	491	35.4	205	1	W96319	bcl-2 polypeptide.	5.46e-35
42	459	33.1	205	1	P80988	Sequence of bcl-2-beta	6.19e-32
43	418	30.2	229	1	W94348	Human Bcl-2 mutant pro	4.84e-28
44	418	30.2	229	1	W01021	Apoptosis-blocking pro	4.84e-28
45	330	23.8	63	1	R68885	Human thymus BCL-X1.	8.75e-20

ALIGNMENTS

RESULT 1
ID Y05533 standard; Protein; 192 AA.
AC Y05533;
DT 05-JUL-1999 (first entry)
DE Mouse Bcl-w protein deritvative.
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
OS Mus sp.
PN WO9913710-A1.
PD 25-MAR-1999.
PF 16-SEP-1998; AU0764.
PR 16-SEP-1997; AU-009228.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
DR WPI; 99-243890/20.
DR N-PSDB; X25135.
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
PS Disclosure; Page 39; 52pp; English.
CC The present sequence is described of a derivative of mouse Bcl-w
CC (see also Y05531), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
SQ Sequence 192 AA;

Query Match 100.0%; Score 1386; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 8.04e-123;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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RA   HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RA   NAKAYAMA K., NAKAYAMA K.-I.;
RL   Int. Immunol. 0:0-0(1998).
DR   EMBL; U23781; AAB97956.1; -.
DR   EMBL; U23780; AAB97956.1; JOINED.
DR   MGD; MGI:1278325; Bcl2ald.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   172 AA;  20048 MW;  1B340DDD CRC32;

  Query Match           11.6%;  Score 162;  DB 11;  Length 172;
  Best Local Similarity  32.6%;  Pred. No. 8.16e-11;
  Matches   28;  Conservative   20;  Mismatches  31;  Indels   7;  Gaps   5;

Db     58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
          ::|| :  :|:  | || :  |: |  ||||:|::| ||: |    :  |  :| ||
Qy     67 QLHVTP-GSAQQRFTQVSDELFQGGP-NWGRLVAFFLFGAALCAESVNKEMEPL-VG--- 120

Db    117 QVSSFVAEFIMNNTGEWIRRNGGWED 142
          ||   :  ::     :||: :||| :
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAE 146


RESULT   13
ID   Q9W6F1      PRELIMINARY;      PRT;   211 AA.
AC   Q9W6F1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 99190706.
RA   LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
RT   "Role of Nr13 in regulation of programmed cell death in the bursa of
RT   Fabricius.";
RL   Genes Dev. 13:718-728(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SOFER L., BURNSIDE J.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF120210; AAD31644.1; -.
DR   PROSITE; PS01080; BH1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   211 AA;  23143 MW;  DEE4E997 CRC32;

  Query Match           11.2%;  Score 156;  DB 13;  Length 211;
  Best Local Similarity  22.0%;  Pred. No. 8.69e-10;
  Matches   29;  Conservative   32;  Mismatches  70;  Indels   1;  Gaps   1;

Db     55 PGRASSAVMEKALETLRRVGDGVMQKHELAFQGMLRKLEIKKEDDLQAVCEVAAQVFNDG 114
          :| : ::  :   :::|  ||    :  :|  :   | :      |   :|: ::|  |
Qy     31 AGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90

Db    115 VTNWGRVVTLISFGAFVAKHLKSINQEKCITSLAGIITDALVSSKREWLMSQGGWEGFVD 174
            ||||:|::: ||| :     : : |  :  :   :   | :   :|: | |||  |
Qy     91 -PNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149

Db    175 FFRVEDLESSIR 186
          ::    || : |
Qy    150 LYGDGALEEARR 161


RESULT   14
ID   O77738      PRELIMINARY;      PRT;    80 AA.
AC   O77738;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BAK PROTEIN (FRAGMENT).
GN   BAK.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ001204; CAA04598.1; -.
DR   HSSP; Q16611; 1BXL.
DR   PROSITE; PS01259; BH3; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   NON_TER       1      1
FT   NON_TER      80     80
SQ   SEQUENCE   80 AA;  8818 MW;  973BE2D0 CRC32;

  Query Match           10.3%;  Score 144;  DB 6;  Length 80;
  Best Local Similarity  35.4%;  Pred. No. 8.91e-08;
  Matches   17;  Conservative   15;  Mismatches  16;  Indels   0;  Gaps   0;

Db     33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
          ||::: |:   |  :  :|: |: :| : || ::  ||::| ||||:|
Qy     50 GDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLV 97


RESULT   15
ID   Q9Y3R2      PRELIMINARY;      PRT;   923 AA.
AC   Q9Y3R2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   NUCLEAR TRANSPORT RECEPTOR.
GN   MTR10A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KUTAY U., IZAURRALDE E., HARTMANN E., GOERLICH D.;
RT   "A human homologue of yeast Mtr10p and its role in nuclear protein
RT   import.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ133769; CAB42643.1; -.
KW   Receptor.
SQ   SEQUENCE   923 AA;  104203 MW;  1661174C CRC32;

  Query Match            8.5%;  Score 119;  DB 4;  Length 923;
  Best Local Similarity  32.9%;  Pred. No. 8.14e-04;
  Matches   28;  Conservative   15;  Mismatches  39;  Indels   3;  Gaps   3;

Db    383 EPDHEGVPEETDDFGE-FRMRVSDLVKDLIFLIGSME-CFAQLYSTLKEGNPPWE-VTEA 439
          :| |:::    |:|   ||   |||  :|    || :  |:|:   | :| | |  :
Qy     40 DPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAF 99

Db    440 VLFIMAAIAKSVDPENNPTLVEVLE 464
          ||  |  | ||: | :| : :| |
Qy    100 FLFGAALCAESVNKEMEPLVGQVQE 124


Search completed: Fri Jun 23 14:15:48 2000
Job time : 36 secs.
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          ::|:::  :|:|  : |     ::|  : : :  ::   |  |::  |||::
Qy     95 RLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAE 146


RESULT    9
ID   P97287      PRELIMINARY;      PRT;   331 AA.
AC   P97287;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   EAT/MCL-1 PROTEIN (MCL1).
GN   EAT/MCL-1 OR MCL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98322120.
RA   OKITA H., UMEZAWA A., SUZUKI A., HATA J.;
RT   "Up-regulated expression of murine Mcl1/EAT, a bcl-2 related gene, in
RT   the early stage of differentiation of murine embryonal carcinoma cells
RT   and embryonic stem cells.";
RL   Biochim. Biophys. Acta 1398:335-341(1998).
RN   [2]
RP   SEQUENCE OF 1-65 FROM N.A.
RC   STRAIN=129/SVJ;
RX   MEDLINE; 98336293.
RA   CHAO J.R., WANG J.M., LEE S.F., PENG H.W., LIN Y.H., CHOU C.H.,
RA   LI J.C., HUANG H.M., CHOU C.K., KUO M.L., YEN J.J.Y., YANG-YEN H.F.;
RT   "mcl-1 is an immediate-early gene activated by the granulocyte-
RT   macrophage colony-stimulating factor (GM-CSF) signaling pathway and is
RT   one component of the GM-CSF viability response.";
RL   Mol. Cell. Biol. 18:4883-4898(1998).
DR   EMBL; U35623; AAC31790.1; -.
DR   EMBL; AF063886; AAC27929.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:101769; Mcl1.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   331 AA;  35217 MW;  3103C5FE CRC32;

  Query Match           12.0%;  Score 167;  DB 11;  Length 331;
  Best Local Similarity  25.2%;  Pred. No. 1.11e-11;
  Matches   33;  Conservative   30;  Mismatches  64;  Indels   4;  Gaps   4;

Db    181 GEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIKNEGDVKSFSRVMVHVFKDGVT 240
          || |:|:    :::|  ||  :     :|  :   | :   :    |::|   :|  |
Qy     34 GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG-P 91

Db    241 NWGRIVTLISFGA-FVAKHLKSVNQESFIEPLAETITDVLVRTKRDWLVKQRGWDGFVEF 299
          ||||:|:::  ||| : |  ::  : |:::  : | :   |     ||:    ||  |  :
Qy     92 NWGRLVAFFLFGAALCAESVNK-EMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTAL 150

Db    300 FHVQDLEGGIR 310
          :    || : |
Qy    151 YGDGALEEARR 161


RESULT   10
ID   Q9Z1P3      PRELIMINARY;      PRT;   330 AA.
AC   Q9Z1P3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MCL-1 PROTEIN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LEO C.P., HSU S.Y., HSUEH A.J.W.;
RT   "Sequence of rat Mcl-1, a Bcl-2-related gene.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF115380; AAD13295.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   PROSITE; PS01080; BH1; 1.
SQ   SEQUENCE   330 AA;  35195 MW;  CC87F2E0 CRC32;

  Query Match           11.8%;  Score 165;  DB 11;  Length 330;
  Best Local Similarity  24.5%;  Pred. No. 2.47e-11;
  Matches   37;  Conservative   33;  Mismatches  75;  Indels   6;  Gaps   6;

Db    160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
          :::: | ||: :     | | || |:|:    :::|  ||  :     :|  :   | :
Qy     16 DFVG-YKLRQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71

Db    219 NEDDVKSFSRVMTHVFKDGVTNWGRIVTLISFGAFVAKHLKSINQESCIEPLAESITDVL 278
              |::|   :|  |  ||||:|::: ||| :     : : |: :  : | :   |
Qy     72 PGSAQQRFTQVSDELFQGG-PNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYL 130

Db    279 VRTKRDWLVKQRGWDGFVEFFHVQDLEGGIR 309
              ||:    ||  |  ::    || : |
Qy    131 ETRLVDWIHSSGGWAEFTALYGDGALEEARR 161


RESULT   11
ID   O55177      PRELIMINARY;      PRT;   172 AA.
AC   O55177;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN A1B (A1-B PROTEIN).
GN   BCL2A1B OR A1B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=LIVER;
RA   HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RA   NAKAYAMA K., NAKAYAMA K.-I.;
RL   Int. Immunol. 0:0-0(1998).
DR   EMBL; U23778; AAB97954.1; -.
DR   EMBL; U23777; AAB97954.1; JOINED.
DR   MGD; MGI:1278326; Bcl2a1b.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   172 AA;  20048 MW;  FA16DF6C CRC32;

  Query Match           11.7%;  Score 163;  DB 11;  Length 172;
  Best Local Similarity  32.6%;  Pred. No. 5.48e-11;
  Matches   28;  Conservative   20;  Mismatches  31;  Indels   7;  Gaps   5;

Db     58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
          ::|| :  :|:  | || :  |: |  ||||:|::| ||: |    :  |  :| ||
Qy     67 QLHVTP-GSAQQRFTQVSDELFQGGP-NWGRLVAFFLFGAALCAESVNKEMEPL-VG--- 120

Db    117 QVSSFVAEFIINNTGEWIRRNGGWED 142
          ||   :  ::     :||: :||| :
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAE 146


RESULT   12
ID   O55179      PRELIMINARY;      PRT;   172 AA.
AC   O55179;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN A1D (A1-D PROTEIN).
GN   BCL2A1D OR A1D.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=LIVER;
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RA   HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF136230; AAD33683.1; -.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
SQ   SEQUENCE   170 AA;  19031 MW;  8B29C9C1 CRC32;

  Query Match           14.8%;  Score 207;  DB 11;  Length 170;
  Best Local Similarity  58.3%;  Pred. No. 6.91e-19;
  Matches   28;  Conservative   11;  Mismatches   8;  Indels   1;  Gaps   1;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
          :: ||:| |||||| |:||:||||::|||:|||:| | | | |  :|:
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVS-DELF 87


RESULT    6
ID   O35425      PRELIMINARY;      PRT;   213 AA.
AC   O35425;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   BCL-2-RELATED OVARIAN KILLER PROTEIN.
GN   BOK OR MTD.
OS   Rattus norvegicus (Rat), and Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, UTERUS;
RX   MEDLINE; 98024143.
RA   HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.W.;
RT   "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT   reproductive tissues and heterodimerizes with selective anti-apoptotic
RT   Bcl-2 family members.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, UTERUS;
RA   HSU S.Y., HSUEH A.J.W.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=MOUSE;
RA   INOHARA N., EKHTERAE D., GARCIA I., CARRIO R., MERINO J., MERRY A.,
RA   CHEN S., NUNEZ G.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF027954; AAB87418.1; -.
DR   EMBL; AF027707; AAC53582.1; -.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   213 AA;  23456 MW;  29761D17 CRC32;

  Query Match           12.5%;  Score 175;  DB 11;  Length 213;
  Best Local Similarity  24.8%;  Pred. No. 4.38e-13;
  Matches   25;  Conservative   33;  Mismatches  38;  Indels   5;  Gaps   5;

Db     75 GDELE-QIRPSVYRNVARQLHIPLQSEPVVTDAFLAVAGHIFSAGITWGKVVSLYSVAAG 133
          |||:| ::| : : ::| |||:   : :   : |  |:  :| :|  ||::|:::  :|:
Qy     50 GDEFETRFRRT-FSDLAAQLHVT-PG-SA-QQRFTQVSDELFQGGPNWGRLVAFFLFGAA 105

Db    134 LAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 174
          |  : |     ::|  : : :  ::   |  |::  |||::
Qy    106 LCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAE 146


RESULT    7
ID   Q9W6F2      PRELIMINARY;      PRT;   174 AA.
AC   Q9W6F2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   PROTEIN A1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 99190706.
RA   LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
RT   "Role of Nr13 in regulation of programmed cell death in the bursa of
RT   Fabricius.";
RL   Genes Dev. 13:718-728(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SOFER L., BURNSIDE J.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF120211; AAD31645.1; -.
SQ   SEQUENCE   174 AA;  20095 MW;  70F5FDAA CRC32;

  Query Match           12.2%;  Score 170;  DB 13;  Length 174;
  Best Local Similarity  20.4%;  Pred. No. 3.32e-12;
  Matches   30;  Conservative   46;  Mismatches  65;  Indels   6;  Gaps   5;

Db     27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNTNW 86
          |||   : : :|  :  :: :   ::  :  :: :|:     | |  | :| | :|  ||
Qy     36 GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR-FTQVSDELF-QGGPNW 93

Db     87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKE-KISYFITEYI--INNKAAWIDANGGWEN 142
          ||::::| ||: | :  :      | |:  | :::|: |  :  |:: ::| :  :   :
Qy     94 GRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGD 153

Db    143 GFLTKFERRSPLSFSTITDIFAAVLSL 169
          | |    |    : :::  :::: ::|
Qy    154 GALEEARRLREGNWASVRTVLTGAVAL 180


RESULT    8
ID   O88857      PRELIMINARY;      PRT;   170 AA.
AC   O88857;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   BCL-2-RELATED OVARIAN KILLER PROTEIN.
GN   BOK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY, UTERUS;
RX   MEDLINE; 98024143.
RA   HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.;
RT   "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT   reproductive tissues and heterodimerizes with selective anti-apoptotic
RT   Bcl-2 family members.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY, UTERUS;
RA   HSU S.Y., HSUEH A.J.W.;
RT   "A splicing variant of the Bcl-2 member Bok with a truncated BH3
RT   domain induces apoptosis without dimerization with anti-apoptotic Bcl-
RT   2 proteins.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF051093; AAC61928.1; -.
SQ   SEQUENCE   170 AA;  18729 MW;  79B4BBE6 CRC32;

  Query Match           12.1%;  Score 169;  DB 11;  Length 170;
  Best Local Similarity  22.3%;  Pred. No. 4.97e-12;
  Matches   25;  Conservative   37;  Mismatches  48;  Indels   2;  Gaps   2;

Db     21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
          :|:   |    :| | |:  :|: |:    :|  : :|::: |:::|   |:: |  ||
Qy     36 GPAADPLHQAMRAAGDEF-ETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94

Db     80 KVVSLYSVAAGLAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 131
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Qy    181 GALVTVGAFFASK 193


RESULT    2
ID   O35844      PRELIMINARY;      PRT;   233 AA.
AC   O35844;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL2-LIKE (BCL-XL).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   YANG X.-F., WEBER G.F., CANTOR H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51278; AAC53459.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   233 AA;  26033 MW;  A4A14278 CRC32;

  Query Match           45.1%;  Score 630;  DB 11;  Length 233;
  Best Local Similarity  53.8%;  Pred. No. 1.97e-106;
  Matches   78;  Conservative   30;  Mismatches  35;  Indels   2;  Gaps   2;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
           ||:||| |||:|||: ||:::  || :||: :|  ||: :|||  |  |||: |  |:|
Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db    205 KGKEGFNRWFLTGMTVAGVVLLGSL 229
          : :|| | |      ::| | ||:|
Qy    161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    3
ID   O02718      PRELIMINARY;      PRT;   229 AA.
AC   O02718;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL-2 (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN; TISSUE=THYMUS;
RA   REYES R.A., COCKERELL G.L.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92434; AAB53319.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
FT   NON_TER     229    229

SQ   SEQUENCE   229 AA;  25099 MW;  E82B3DFB CRC32;

  Query Match           42.2%;  Score 590;  DB 6;  Length 229;
  Best Local Similarity  44.5%;  Pred. No. 9.22e-98;
  Matches   73;  Conservative   46;  Mismatches  40;  Indels   5;  Gaps   3;

Db     71 AAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFRD 130
          :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|::||: | :|||:
Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    131 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFVE 190
          | ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :|  ||: :|||  |
Qy     90 GPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149

Db    191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
          |||  ::   | | : :| |::::|: |: :|| :|:||::: |
Qy    150 LYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT    4
ID   O35843      PRELIMINARY;      PRT;   235 AA.
AC   O35843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL2-LIKE (BCL-X-GAMMA).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   YANG X.-F., WEBER G.F., CANTOR H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51277; AAC53458.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   235 AA;  26122 MW;  FB0B0207 CRC32;

  Query Match           38.3%;  Score 535;  DB 11;  Length 235;
  Best Local Similarity  59.0%;  Pred. No. 6.46e-86;
  Matches   62;  Conservative   24;  Mismatches  19;  Indels   0;  Gaps   0;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWG 189
           ||:||| |||:|||: ||:::  || :||: :|  ||: :|||:
Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWA 145


RESULT    5
ID   Q9WUI5      PRELIMINARY;      PRT;   170 AA.
AC   Q9WUI5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL-X SHORT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
```

****

MPSRCH (TM)

****

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:15:12 2000; MasPar time 18.46 Seconds
724.726 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 44.702; Variance 83.297; scale 0.537

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1378	98.6	193	11	O88996	BCL-W.	5.72e-273
2	630	45.1	233	11	O35844	BCL2-LIKE (BCL-XL).	1.97e-106
3	590	42.2	229	6	O02718	BCL-2 (FRAGMENT).	9.22e-98
4	535	38.3	235	11	O35843	BCL2-LIKE (BCL-X-GAMMA	6.46e-86
5	207	14.8	170	11	Q9WUI5	BCL-X SHORT.	6.91e-19
6	175	12.5	213	11	O35425	BCL-2-RELATED OVARIAN	4.38e-13
7	170	12.2	174	13	Q9W6F2	PROTEIN A1.	3.32e-12
8	169	12.1	170	11	O88857	BCL-2-RELATED OVARIAN	4.97e-12
9	167	12.0	331	11	P97287	EAT/MCL-1 PROTEIN (MCL	1.11e-11
10	165	11.8	330	11	Q9Z1P3	MCL-1 PROTEIN.	2.47e-11
11	163	11.7	172	11	O55177	B-CELL LEUKEMIA/LYMPHO	5.48e-11
12	162	11.6	172	11	O55179	B-CELL LEUKEMIA/LYMPHO	8.16e-11
13	156	11.2	211	13	Q9W6F1	MYELOID CELL LEUKEMIA	8.69e-10
14	144	10.3	80	6	O77738	BAK PROTEIN (FRAGMENT)	8.91e-08
15	119	8.5	923	4	Q9Y3R2	NUCLEAR TRANSPORT RECE	8.14e-04
16	117	8.4	128	11	O55178	B-CELL LEUKEMIA/LYMPHO	1.63e-03
17	103	7.4	1259	5	O44971	C42C1.4 PROTEIN.	1.72e-01
18	102	7.3	451	2	O69657	HYPOTHETICAL 46.4 KD P	2.36e-01
19	102	7.3	975	4	Q9Y5L0	TRANSPORTIN-SR.	2.36e-01
20	100	7.2	168	14	O36423	SIMILAR TO BCL-FAMILY	4.44e-01
21	101	7.2	378	2	O53318	HYPOTHETICAL 42.6 KD P	3.24e-01
22	100	7.2	440	1	Q9YFI3	440AA LONG HYPOTHETICA	4.44e-01
23	100	7.2	451	5	P90814	F46C5.9 PROTEIN.	4.44e-01
24	100	7.2	505	1	O27209	CONSERVED PROTEIN (FLP	4.44e-01
25	100	7.2	505	1	Q50517	HYPOTHETICAL 55.1 KD P	4.44e-01
26	99	7.1	967	5	Q18965	D2013.5 PROTEIN.	6.07e-01
27	98	7.0	521	14	Q9YTU1	GAG PROTEIN.	8.28e-01
28	98	7.0	572	5	Q19345	NHR-25 PROTEIN.	8.28e-01
29	98	7.0	579	14	Q65605	SURFACE ENVELOPE PROTE	8.28e-01
30	96	6.9	757	14	O37361	PUTATIVE RNA DEPENDENT	1.53e+00
31	95	6.8	130	14	P87527	SURFACE ENVELOPE PROTE	2.07e+00
32	95	6.8	148	14	P87532	SURFACE ENVELOPE PROTE	2.07e+00
33	95	6.8	148	14	P87531	SURFACE ENVELOPE PROTE	2.07e+00
34	95	6.8	256	2	Q9Z657	MORPHINE 6-DEHYDROGENA	2.07e+00
35	95	6.8	597	14	Q9YUR4	TERMINAL PROTEIN.	2.07e+00
36	95	6.8	630	5	Q24222	METALLOPEPTIDASE.	2.07e+00
37	95	6.8	668	2	Q51711	CYTOCHROME BA (EC 1.9.	2.07e+00
38	95	6.8	1053	2	P77865	ENDOGLUCANASE F PRECUR	2.07e+00
39	93	6.7	130	14	P87529	SURFACE ENVELOPE PROTE	3.78e+00
40	93	6.7	131	14	P90358	SURFACE ENVELOPE PROTE	3.78e+00
41	94	6.7	279	14	O57148	SEROTYPE B PUTATIVE MA	2.80e+00
42	93	6.7	576	14	Q65604	SURFACE ENVELOPE PROTE	3.78e+00
43	94	6.7	585	14	Q65603	SURFACE ENVELOPE PROTE	2.80e+00
44	94	6.7	896	1	O30061	MOLYBDOPTERIN OXIDORED	2.80e+00
45	93	6.7	1937	2	O30482	PKS MODULE 4.	3.78e+00

ALIGNMENTS

RESULT 1
ID O88996 PRELIMINARY; PRT; 193 AA.
AC O88996;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE BCL-W.
GN BCL-W.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA HAMNER S., SKOGLOSA Y., LINDHOLM D.;
RT "Differential expression of Bcl-w and Bcl-x mRNA in the developing and
RT adult nervous system.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF096291; AAC64200.1; -.
DR HSSP; P53563; 1AF3.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PFAM; PF00452; Bcl-2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 6E5F84BA CRC32;

Query Match 98.6%; Score 1378; DB 11; Length 193;
Best Local Similarity 97.4%; Pred. No. 5.72e-273;
Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
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RESULT   14
ENTRY            D37332     #type complete
TITLE            transforming protein (bcl-2-beta) - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                   23-Feb-1997
ACCESSIONS       D37332
REFERENCE        A37332
   #authors      Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal      Nucleic Acids Res. (1992) 20:4187-4192
   #title        Isolation and characterization of the chicken bcl-2 gene:
                   expression in a variety of tissues including lymphoid and
                   neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession    D37332
      ##status        preliminary; nucleic acid sequence not shown; not
                        compared with conceptual translation
      ##molecule_type DNA
      ##residues      1-206 ##label EGU
CLASSIFICATION   #superfamily bcl transforming protein
KEYWORDS         mitochondrion
SUMMARY          #length 206  #molecular-weight 22440  #checksum 5581

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  Best Local Similarity  49.6%;  Pred. No. 1.33e-76;
  Matches    57;  Conservative   29;  Mismatches  29;  Indels   0;  Gaps   0;

Db      82 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 141
           :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy      30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db     142 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 196
           | ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :|  ||: :|||
Qy      90 GPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGW 144


RESULT   15
ENTRY            TVMSB1     #type complete
TITLE            transforming protein bcl-2-beta - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                   18-Jun-1999
ACCESSIONS       B25960
REFERENCE        A90893
   #authors      Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                   C.M.
   #journal      Cell (1987) 49:455-463
   #title        Molecular analysis of mbcl-2: structure and expression of the
                   murine gene homologous to the human gene involved in
                   follicular lymphoma.
   #cross-references MUID:87187643
   #accession    B25960
      ##molecule_type DNA
      ##residues      1-199 ##label NEG
      ##cross-references GB:M16506; NID:g468335; PIDN:AAA37281.1; PID:g387110
GENETICS
   #gene         BCL2
CLASSIFICATION   #superfamily bcl transforming protein
KEYWORDS         alternative splicing; transforming protein
SUMMARY          #length 199  #molecular-weight 22299  #checksum 7397

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  Best Local Similarity  49.6%;  Pred. No. 3.39e-76;
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Db      76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 192
           : | ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :|  ||: :|||
Qy      88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGW 144
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Search completed: Fri Jun 23 14:14:23 2000
Job time : 20 secs.

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   #title        Molecular cloning and DNA sequence analysis of cDNA encoding
                   chicken homologue of the Bcl-2 oncoprotein.
   #cross-references MUID:92379084
   #accession    S24390
      ##status       preliminary
      ##molecule_type mRNA
      ##residues     1-232 ##label CAZ
      ##cross-references EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
CLASSIFICATION   #superfamily bcl transforming protein
KEYWORDS         mitochondrion; transmembrane protein
SUMMARY          #length 232  #molecular-weight 25839  #checksum 1516

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  Matches    74;  Conservative   38;  Mismatches  41;  Indels   6;  Gaps   4;

Db      79 GCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEELFRDGVNWV 138
           | || | :| |:| |||||  |::| |:::::|||:|| :|  ||  | :|||: | ||
Qy      36 GPAADP-LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94

Db     139 RIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN- 197
           |:|||| ||: :| ||||:|| |||  :  ||  ||: :| :||: :|||  |  |||:
Qy      95 RLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDG 154

Db     198 SM---RPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232
           ::   | | : :| |::|:|:  | :|| :|:||::: |
Qy     155 ALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   11
ENTRY            I49057     #type complete
TITLE            bcl-x transmembrane deleted - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                   16-Jul-1999
ACCESSIONS       I49057
REFERENCE        I49055
   #authors      Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
   #journal      J. Immunol. (1994) 153:4388-4398
   #title        Cloning and molecular characterization of mouse bcl-x in B
                   and T lymphocytes.
   #cross-references MUID:95052604
   #accession    I49057
      ##status       preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues     1-214 ##label RES
      ##cross-references EMBL:U10102; NID:g506649; PIDN:AAA82174.1;
                        PID:g506650
GENETICS
   #gene         bcl-x-long
CLASSIFICATION   #superfamily bcl transforming protein
SUMMARY          #length 214  #molecular-weight 23900  #checksum 9730

  Query Match           38.9%;  Score 543;  DB 2;  Length 214;
  Best Local Similarity  58.9%;  Pred. No. 4.13e-83;
  Matches    63;  Conservative   23;  Mismatches  21;  Indels   0;  Gaps   0;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTF 191
           ||:||| |||:|||: ||::  || :||: :|  ||: :|||  |
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147


RESULT   12
ENTRY            JE0203     #type complete
TITLE            apoptosis regulator bcl-x isoform - human
ALTERNATE_NAMES  h-bcl-xbeta
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
                   16-Jul-1999
ACCESSIONS       JE0203
REFERENCE        JE0203
   #authors      Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
                   E.
   #journal      Biochem. Biophys. Res. Commun. (1998) 248:147-152
   #title        Identification of a human cDNA encoding a novel bcl-x
                   isoform.
   #cross-references MUID:98340865
   #accession    JE0203
      ##molecule_type mRNA
      ##residues     1-227 ##label BAN
      ##cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1;
                        PID:g1622941
GENETICS
   #gene         bcl-x
   #map_position 20
CLASSIFICATION   #superfamily bcl transforming protein
SUMMARY          #length 227  #molecular-weight 25290  #checksum 864

  Query Match           38.5%;  Score 538;  DB 2;  Length 227;
  Best Local Similarity  53.7%;  Pred. No. 4.32e-82;
  Matches    65;  Conservative   27;  Mismatches  29;  Indels   0;  Gaps   0;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWVRTKPLVCPFSLASGQ 204
           ||:||| |||:|||: ||::  || :||: :|  ||: :|||    :|    :|  ::
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 R 205
           |
Qy     161 R 161


RESULT   13
ENTRY            A47537     #type complete
TITLE            apoptosis regulator bcl-x - chicken
ORGANISM         #formal_name Gallus gallus #common_name chicken
DATE             03-May-1994 #sequence_revision 03-May-1994 #text_change
                   16-Jul-1999
ACCESSIONS       A47537
REFERENCE        A47537
   #authors      Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
                   Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                   C.B.
   #journal      Cell (1993) 74:597-608
   #title        bcl-x, a bcl-2-related gene that functions as a dominant
                   regulator of apoptotic cell death.
   #cross-references MUID:93364977
   #accession    A47537
      ##status       preliminary
      ##molecule_type DNA
      ##residues     1-190 ##label BOI
      ##cross-references GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
                        PID:g510899
CLASSIFICATION   #superfamily bcl transforming protein
SUMMARY          #length 190  #molecular-weight 21467  #checksum 5509

  Query Match           38.4%;  Score 537;  DB 2;  Length 190;
  Best Local Similarity  59.8%;  Pred. No. 6.90e-82;
  Matches    67;  Conservative   20;  Mismatches  24;  Indels   1;  Gaps   1;

Db      79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
           |  ::||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||
Qy      39 ADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVA 98

Db     139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWVR-TAL 189
           || ||:||| |||:|||  |||::  || :||  :|  ||: :|||   |||
Qy      99 FFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTAL 150
```

```
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              29-May-1998 #sequence_revision 29-May-1998 #text_change
                    16-Jul-1999
ACCESSIONS        I53744
REFERENCE         I53744
   #authors       Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
   #journal       Gene (1994) 140:291-292
   #title         Cloning and sequencing of a cDNA encoding the rat Bcl-2
                    protein.
   #cross-references MUID:94193015
   #accession     I53744
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-236 ##label RES
      ##cross-references GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
GENETICS
   #gene          bcl-2
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 236  #molecular-weight 26550  #checksum 8001

  Query Match             41.4%;  Score 579;  DB 2;  Length 236;
  Best Local Similarity   44.6%;  Pred. No. 1.80e-90;
  Matches    74;  Conservative    43;  Mismatches  44;  Indels    5;  Gaps    3;

Db      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :|  |||:|| |||  :  ||  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
             |||  ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy     148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT    8
ENTRY             I67431     #type complete
TITLE             BCL-X-Long - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I67431
REFERENCE         I53295
   #authors       Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
   #journal       Endocrinology (1995) 136:232-241
   #title         Expression of members of the bcl-2 gene family in the
                    immature rat ovary: equine chorionic gonadotropin-mediated
                    inhibition of granulosa cell apoptosis is associated with
                    decreased bax and constitutive bcl-2 and bcl-xlong
                    messenger ribonucleic acid levels.
   #cross-references MUID:95129487
   #accession     I67431
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-233 ##label RES
      ##cross-references EMBL:U34963; NID:g1004376; PIDN:AAA77686.1;
                          PID:g1004377
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 233  #molecular-weight 26122  #checksum 8310

  Query Match             41.3%;  Score 577;  DB 2;  Length 233;
  Best Local Similarity   50.3%;  Pred. No. 4.62e-90;
  Matches    73;  Conservative    31;  Mismatches  39;  Indels    2;  Gaps    2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFEQVVNELFRDGVNWGRIVASS 144
           :: ||:| |||||| |:||:||||::|||:|||:  | | || :|||: | ||||:||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNTAPESR 204
           ||:||| |||:|||: ||::  || :||: :|  ||: :|||  |  |||: :  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    9
ENTRY             TVMSA1     #type complete
TITLE             transforming protein bcl-2-alpha - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                    18-Jun-1999
ACCESSIONS        A25960; E37332
REFERENCE         A90893
   #authors       Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                    C.M.
   #journal       Cell (1987) 49:455-463
   #title         Molecular analysis of mbcl-2: structure and expression of the
                    murine gene homologous to the human gene involved in
                    follicular lymphoma.
   #cross-references MUID:87187643
   #accession     A25960
      ##molecule_type DNA
      ##residues       1-236 ##label NEG
      ##cross-references GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1;
                          PID:g387109
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
                    neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession     E37332
      ##status         preliminary; nucleic acid sequence not shown; not
                          compared with conceptual translation
      ##molecule_type DNA
      ##residues       1-33,'E',34-220,'AL',223-236 ##label EGU
GENETICS
   #gene          BCL2
   #introns       192/3
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          alternative splicing; mitochondrion; transforming protein;
                    transmembrane protein
SUMMARY           #length 236  #molecular-weight 26524  #checksum 6709

  Query Match             40.9%;  Score 572;  DB 1;  Length 236;
  Best Local Similarity   44.6%;  Pred. No. 4.89e-89;
  Matches    74;  Conservative    43;  Mismatches  44;  Indels    5;  Gaps    3;

Db      76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| |||  :  ||  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLP-WVGACITLGAYLGHK 236
             |||  ::   | | : :| |::|:|: :  :|| :|:||::: |
Qy     148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT   10
ENTRY             S24390     #type complete
TITLE             transforming protein (Bcl-2) homolog - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                    16-Jul-1999
ACCESSIONS        S24390
REFERENCE         S24390
   #authors       Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
   #journal       Biochim. Biophys. Acta (1992) 1132:109-113
```

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          ||: ::   | | : :| |::|:|:  | :|| :|:||::: |
Qy    151 YGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT    5
ENTRY             TVHUA1     #type complete
TITLE             transforming protein bcl-2, splice form alpha - human
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change
                    18-Jun-1999
ACCESSIONS        C37332; A29409; S02452; A24428; A27622; B27622
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
                    neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession     C37332
      ##status         nucleic acid sequence not shown; not compared with
                         conceptual translation
      ##molecule_type DNA
      ##residues       1-239 ##label EGU
      ##note           this report is a correction
REFERENCE         A29409
   #authors       Tsujimoto, Y.; Croce, C.M.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
   #title         Analysis of the structure, transcripts, and protein products
                    of bcl-2, the gene involved in human follicular lymphoma.
   #cross-references MUID:86259760
   #accession     A29409
      ##molecule_type mRNA
      ##residues       1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
      ##cross-references GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
      ##note           this sequence has been corrected in reference A37332
REFERENCE         S02452
   #authors       Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
                    S.; Goldman, P.; Korsmeyer, S.J.
   #journal       EMBO J. (1988) 7:123-131
   #title         Alternative promoters and exons, somatic mutation and
                    deregulation of the Bcl-2--Ig fusion gene in lymphoma.
   #cross-references MUID:88196071
   #accession     S02452
      ##molecule_type mRNA
      ##residues       1-239 ##label SET
REFERENCE         A24428
   #authors       Cleary, M.L.; Smith, S.D.; Sklar, J.
   #journal       Cell (1986) 47:19-28
   #title         Cloning and structural analysis of cDNAs for bcl-2 and a
                    hybrid bcl-2/immunoglobulin transcript resulting from the t
                    (14;18) translocation.
   #cross-references MUID:87002488
   #accession     A24428
      ##molecule_type mRNA
      ##residues       1-58,'T',60-116,'R',118-239 ##label CLE
      ##cross-references GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
REFERENCE         A27622
   #authors       Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.;
                    Wright, J.J.; Bakhshi, A.
   #journal       Oncogene Res. (1988) 2:263-275
   #title         Consequences of the t(14;18) chromosomal translocation in
                    follicular lymphoma: deregulated expression of a chimeric
                    and mutated BCL-2 gene.
   #cross-references MUID:88217344
   #accession     A27622
      ##molecule_type mRNA
      ##residues       1-58,'T',60-239 ##label HUA
   #accession     B27622
      ##molecule_type DNA
      ##residues       1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2
      ##note           the sequence was determined from the germline gene
COMMENT     Constitutive expression of BCL2 following t(14:18) chromosomal
              translocation is typically found in follicular lymphoma.
GENETICS
   #gene          GDB:BCL2
      ##cross-references GDB:119031; OMIM:151430
   #map_position 18q21.3-18q21.3
FUNCTION
   #description   blocks apoptosis in hematopoietic cells
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          alternative splicing; B-cell lymphoma; follicular lymphoma;
                    proto-oncogene; transforming protein; transmembrane protein
SUMMARY           #length 239  #molecular-weight 26266  #checksum 8323

  Query Match             41.9%;  Score 586;  DB 1;  Length 239;
  Best Local Similarity   45.1%;  Pred. No. 6.59e-92;
  Matches    74;  Conservative    44;  Mismatches  41;  Indels    5;  Gaps    3;

Db      81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
           :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy      30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db     141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
           | ||||:|||| ||: :| ||||:|| ||| : || ||: :| ||: :||| |
Qy      90 GPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149

Db     201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
           ||| ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy     150 LYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT    6
ENTRY             I67432     #type fragment
TITLE             BCL-2 - rat (fragment)
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I67432
REFERENCE         I53295
   #authors       Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
   #journal       Endocrinology (1995) 136:232-241
   #title         Expression of members of the bcl-2 gene family in the
                    immature rat ovary: equine chorionic gonadotropin-mediated
                    inhibition of granulosa cell apoptosis is associated with
                    decreased bax and constitutive bcl-2 and bcl-xlong
                    messenger ribonucleic acid levels.
   #cross-references MUID:95129487
   #accession     I67432
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-236 ##label RES
      ##cross-references EMBL:U34964; NID:g1004378; PIDN:AAA77687.1;
                          PID:g1004379
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 236  #checksum 9134

  Query Match             41.7%;  Score 583;  DB 2;  Length 236;
  Best Local Similarity   45.2%;  Pred. No. 2.72e-91;
  Matches    75;  Conservative    43;  Mismatches  43;  Indels    5;  Gaps    3;

Db      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| ||| : || ||: :| ||: :|||  |
Qy      88 QGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEF 147

Db     196 VELYGP-SM---RPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
             ||| ::   | | : :| |::|:|: |: :|| :|:||::: |
Qy     148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193


RESULT    7
ENTRY             I53744     #type complete
TITLE             gene bcl-2 protein - rat
```

```
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||::: || :||: :| ||: :||| | |||: | |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :| | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    2
ENTRY             S51761     #type complete
TITLE             BCL-X protein - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              07-May-1995 #sequence_revision 01-Sep-1995 #text_change
                    16-Jul-1999
ACCESSIONS        S51761; S51762
REFERENCE         S51761
   #authors       Michaelidis, T.M.
   #submission    submitted to the EMBL Data Library, November 1994
   #accession     S51761
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-233 ##label MIC
      ##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
                        PID:g607177
REFERENCE         S51761
   #authors       Michaelidis, T.M.
   #submission    submitted to the EMBL Data Library, November 1994
   #accession     S51762
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-125,189-233 ##label MI2
      ##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1;
                        PID:g607178
GENETICS
   #introns       125/3
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 233  #molecular-weight 26130  #checksum 6378

  Query Match           44.0%;  Score 615;  DB 2;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 7.19e-98;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
           ||:||| |||:|||: ||::: || :||: :| ||: :||| | |||: | |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :| | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    3
ENTRY             I49056     #type complete
TITLE             bcl-x long - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I49056; S52866
REFERENCE         I49055
   #authors       Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
   #journal       J. Immunol. (1994) 153:4388-4398
   #title         Cloning and molecular characterization of mouse bcl-x in B
                    and T lymphocytes.
   #cross-references MUID:95052604
   #accession     I49056
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-233 ##label RES
      ##cross-references EMBL:U10101; NID:g506647; PIDN:AAA82173.1;
                        PID:g506648
REFERENCE         S52866
   #authors       Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
   #submission    submitted to the EMBL Data Library, November 1994
   #description   IL-5 inhibits anti-IgM-induced apoptosis in an immature B
                    cell line through inductin of bcl-Xl.
   #accession     S52866
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-233 ##label KAM
      ##cross-references EMBL:X83574; NID:g695622; PIDN:CAA58557.1;
                        PID:g695623
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 233  #molecular-weight 26132  #checksum 5739

  Query Match           44.0%;  Score 615;  DB 2;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 7.19e-98;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
           ||:||| |||:|||: ||::: || :||: :| ||: :||| | |||: | |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :| | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT    4
ENTRY             A37332     #type complete
TITLE             transforming protein (bcl-2-alpha) - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                    23-Feb-1997
ACCESSIONS        A37332; S35453
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
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   #cross-references MUID:92375724
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      ##residues       1-233 ##label EGU
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   #introns       189/3
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          mitochondrion; transforming protein; transmembrane protein
SUMMARY           #length 233  #molecular-weight 25687  #checksum 99

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Db      76 PAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDG 135
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Qy      33 PGEG-PAADP-LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90

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Db     196 YGN-SM---RPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
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****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:14:03 2000; MasPar time 12.24 Seconds
743.766 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 45.096; Variance 88.441; scale 0.510

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	616	44.1	233	2	B47537	apoptosis regulator b	4.47e-98
2	615	44.0	233	2	S51761	BCL-X protein - rat	7.19e-98
3	615	44.0	233	2	I49056	bcl-x long - mouse	7.19e-98
4	587	42.0	233	2	A37332	transforming protein	4.11e-92
5	586	41.9	239	1	TVHUA1	transforming protein	6.59e-92
6	583	41.7	236	2	I67432	BCL-2 - rat (fragment	2.72e-91
7	579	41.4	236	2	I53744	gene bcl-2 protein -	1.80e-90
8	577	41.3	233	2	I67431	BCL-X-Long - rat	4.62e-90
9	572	40.9	236	1	TVMSA1	transforming protein	4.89e-89
10	567	40.6	232	2	S24390	transforming protein	5.16e-88
11	543	38.9	214	2	I49057	bcl-x transmembrane d	4.13e-83
12	538	38.5	227	2	JE0203	apoptosis regulator b	4.32e-82
13	537	38.4	190	2	A47537	apoptosis regulator b	6.90e-82
14	511	36.6	206	2	D37332	transforming protein	1.33e-76
15	509	36.4	199	1	TVMSB1	transforming protein	3.39e-76
16	499	35.7	205	1	TVHUB1	transforming protein	3.59e-74
17	499	35.7	216	2	B37332	transforming protein	3.59e-74
18	402	28.8	154	2	I58194	gene bcl-2 protein -	9.58e-55
19	235	16.8	192	2	D47538	bcl-2-associated prot	7.46e-23
20	228	16.3	143	2	I38921	bcl-2-associated prot	1.37e-21
21	228	16.3	192	2	A47538	bcl-2-associated prot	1.37e-21
22	226	16.2	211	2	S58873	Bak protein - human	3.14e-21
23	225	16.1	133	2	I53295	bcl-2-associated prot	4.75e-21
24	225	16.1	211	2	S58875	cdn-2 protein - human	4.75e-21
25	218	15.6	218	2	B47538	bcl-2-associated prot	8.47e-20
26	205	14.7	170	2	I49055	bcl-x short - mouse	1.68e-17
27	201	14.4	176	2	I67435	gene bcl-xshort prote	8.43e-17
28	183	13.1	177	2	S54778	NR-13 protein - quail	1.06e-13
29	155	11.1	172	2	I49449	hemopoietic-specific	4.63e-09
30	149	10.7	175	2	I39055	Bcl-2 related - human	4.20e-08
31	150	10.7	350	2	A47476	BCL2 homolog MCL1 - h	2.92e-08
32	148	10.6	280	2	A53189	apoptosis suppressor	6.05e-08
33	102	7.3	451	2	B70792	hypothetical protein	3.13e-01
34	100	7.2	168	2	T03168	hypothetical protein	5.69e-01
35	101	7.2	378	2	F70947	hypothetical protein	4.22e-01
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ALIGNMENTS

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CONTAINS          apoptosis regulator bcl-xS
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
                    16-Jul-1999
ACCESSIONS        B47537; C47537
REFERENCE         A47537
   #authors       Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
                    Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                    C.B.
   #journal       Cell (1993) 74:597-608
   #title         bcl-x, a bcl-2-related gene that functions as a dominant
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      ##molecule_type mRNA
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KEYWORDS          alternative splicing; apoptosis
FEATURE
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Query Match 44.1%; Score 616; DB 2; Length 233;
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Matches 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;

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CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
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CC         APPLICATION NUMBER:  US/08/081,448
CC         FILING DATE:  19930622
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  No. 5646008thrup, Thomas E.
CC         REGISTRATION NUMBER:  33,268
CC         REFERENCE/DOCKET NUMBER:  ARCD090
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  312-744-0090
CC         TELEFAX:  312-755-4489
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

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Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


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CC    Sequence 59, Application US/08661479
CC    Patent No. 5834209
CC     GENERAL INFORMATION:
CC       APPLICANT:  KORSMEYER, Stanley J.
CC       TITLE OF INVENTION:  Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC       TITLE OF INVENTION:  REGULATOR
CC       NUMBER OF SEQUENCES:  59
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC         STREET:  379 Lytton Avenue
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  US
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
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CC         APPLICATION NUMBER:  US/08/661,479
CC         FILING DATE:  11-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/333,565
CC         FILING DATE:  31-OCT-1994
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Smith, William M
CC         REGISTRATION NUMBER:  30,223
CC         REFERENCE/DOCKET NUMBER:  15726A-000700
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 326-2400
CC         TELEFAX:  (415) 326-2422
CC     INFORMATION FOR SEQ ID NO:  59:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
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CC         TOPOLOGY:  unknown
CC       MOLECULE TYPE:  peptide
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Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

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Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


Search completed: Fri Jun 23 14:16:17 2000
Job time : 12 secs.
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CC       APPLICANT:  BARR, PHILIP J.
CC       TITLE OF INVENTION:  NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
CC       TITLE OF INVENTION:  ENCODING THE PROTEINS AND METHODS OF USE THEREOF
CC       NUMBER OF SEQUENCES:  22
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  MORRISON & FOERSTER
CC         STREET:  755 Page Mill Road
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
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CC       COMPUTER READABLE FORM:
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CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/320,157
CC         FILING DATE:  07-OCT-1994
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  LEHNHARDT, SUSAN K.
CC         REGISTRATION NUMBER:  33,943
CC         REFERENCE/DOCKET NUMBER:  23647-20007.20
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 813-5600
CC         TELEFAX:  (415) 494-0792
CC         TELEX:  706141
CC     INFORMATION FOR SEQ ID NO:  14:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
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CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

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CC    Patent No. 5622852
CC     GENERAL INFORMATION:
CC       APPLICANT:  KORSMEYER, Stanley J.
CC       TITLE OF INVENTION:  Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC       TITLE OF INVENTION:  REGULATOR
CC       NUMBER OF SEQUENCES:  59
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC         STREET:  379 Lytton Avenue
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CC         STATE:  California
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CC         FILING DATE:  31-OCT-1994
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Smith, William M
CC         REGISTRATION NUMBER:  30,223
CC         REFERENCE/DOCKET NUMBER:  15726A-000700
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 326-2400
CC         TELEFAX:  (415) 326-2422
CC     INFORMATION FOR SEQ ID NO:  59:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  unknown
CC       MOLECULE TYPE:  peptide
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

  Query Match           44.1%;  Score 616;  DB 1;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 6.27e-44;
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Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

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Qy    161 RLREG-N-WASVRTVLTGAVALGAL 183


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CC    Sequence 6, Application US/08081448
CC    Patent No. 5646008
CC     GENERAL INFORMATION:
CC       APPLICANT:  Thompson, Craig B.
CC       APPLICANT:  Boise, Lawrence H.
CC       TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
CC       TITLE OF INVENTION:  Compositions and Methods
CC       NUMBER OF SEQUENCES:  8
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Arnold, White & Durkee
CC         STREET:  321 No. 5646008th Clark Street, Suite 800
CC         CITY:  Chicago
CC         STATE:  IL
CC         COUNTRY:  USA
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CC         STREET:  P.O. Box 4433
CC         CITY:  Houston
CC         STATE:  TX
CC         COUNTRY:  United States of America
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CC         FILING DATE:  22 JUNE 1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  PARKER, David L.
CC         REGISTRATION NUMBER:  32,165
CC         REFERENCE/DOCKET NUMBER:  ARCD090
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  512-320-7200
CC         TELEFAX:  713-789-2679
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

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Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

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Qy    161 RLREG-N-WASVRTVLTGAVALGAL 183


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CC    Patent No. 5834309
CC    Patent No. 5834309 5710045
CC     GENERAL INFORMATION:
CC       APPLICANT:  Thompson, Craig B. B.
CC       APPLICANT:  Boise, Lawrence H.
CC       TITLE OF INVENTION:  VERTEBRATE APOPTOSIS GENE:
CC       TITLE OF INVENTION:  COMPOSITIONS AND METHODS
CC       NUMBER OF SEQUENCES:  18
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Arnold, White & Durkee
CC         STREET:  P.O. Box 4433
CC         CITY:  Houston
CC         STATE:  Texas
CC         COUNTRY:  United States of America
CC         ZIP:  77210
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/470,670A
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/081,448
CC         FILING DATE:  22-JUN-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Highlander, Steven L.
CC         REGISTRATION NUMBER:  37,642
CC         REFERENCE/DOCKET NUMBER:  ARCD:090--1
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (512) 418-3000
CC         TELEFAX:  (512) 474-7577
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

  Query Match           44.1%;  Score 616;  DB 2;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 6.27e-44;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||:::  || :||: :|  ||: :||| |  |||: |  |:|
Qy    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | |      ::| | ||:|
Qy    161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT   12
ID   US-08-471-057-14     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 14, Application US/08471057
XX
CC    Sequence 14, Application US/08471057
CC    Patent No. 6015687
CC     GENERAL INFORMATION:
CC       APPLICANT:  KIEFER, MICHAEL C.
```

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Db      61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db     121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
           ||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy     122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db     181 ALVTVGAFFASK 192
           ||||||||||||
Qy     182 ALVTVGAFFASK 193


RESULT    8
ID   US-08-798-897-5     STANDARD;     PRT;   192 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 5, Application US/08798897
XX
CC    Sequence 5, Application US/08798897
CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  5:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  192 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   192 AA; 20689 MW; 183185 CN;

  Query Match           97.9%;  Score 1367;  DB 1;  Length 192;
  Best Local Similarity  97.4%;  Pred. No. 1.95e-112;
  Matches   187;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;

Db       1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
           |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db      61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db     121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
           ||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy     122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db     181 ALVTVGAFFASK 192
           ||||||||||||
Qy     182 ALVTVGAFFASK 193


RESULT    9
ID   PCT-US95-04600-24     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 24, Application PC/TUS9504600
XX
CC    Sequence 24, Application PC/TUS9504600
CC     GENERAL INFORMATION:
CC       APPLICANT:  LA JOLLA CANCER RESEARCH FOUNDATION
CC       TITLE OF INVENTION:  Interaction of Proteins Involved in
CC       TITLE OF INVENTION:  a Cell Death Pathway
CC       NUMBER OF SEQUENCES:  29
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Campbell and Flores
CC         STREET:  4370 La Jolla Village Drive, Suite 700
CC         CITY:  San Diego
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  92122
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US95/04600
CC         FILING DATE:  12-APR-1995
CC         CLASSIFICATION:
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Imbra, Richard J.
CC         REGISTRATION NUMBER:  37,643
CC         REFERENCE/DOCKET NUMBER:  FP-LJ 1361
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (619) 535-9001
CC         TELEFAX:  (619) 535-8949
CC     INFORMATION FOR SEQ ID NO:  24:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

  Query Match           44.1%;  Score 616;  DB 4;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 6.27e-44;
  Matches    77;  Conservative   30;  Mismatches  36;  Indels   2;  Gaps   2;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||::::  || :||: :|  ||: :||| |  |||: |  |:|
Qy     101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | |      ::| | ||:|
Qy     161 RLREG-N-WASVRTVLTGAVALGAL 183


RESULT   10
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```
Db      1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Qy      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db    121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    182 ALVTVGAFFASK 193
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RESULT 6
ID US-08-798-897-6 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08798897
XX
CC Sequence 6, Application US/08798897
CC Patent No. 5789201
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 192 AA; 20701 MW; 181510 CN;

Query Match 97.9%; Score 1368; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.58e-112;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Qy      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVGQ 121

Db    121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    182 ALVTVGAFFASK 193
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RESULT 7
ID US-08-978-523-5 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 5, Application US/08978523
XX
CC Sequence 5, Application US/08978523
CC Patent No. 5883229
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/978,523
CC FILING DATE: herewith
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140002
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 192 AA; 20689 MW; 183185 CN;

Query Match 97.9%; Score 1367; DB 2; Length 192;
Best Local Similarity 97.4%; Pred. No. 1.95e-112;
Matches 187; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
```

```
Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193
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RESULT 4
ID US-08-978-523-3 STANDARD; PRT; 193 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 3, Application US/08978523
XX
CC Sequence 3, Application US/08978523
CC Patent No. 5883229
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/978,523
CC FILING DATE: herewith
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140002
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 193 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 193 AA; 20820 MW; 185063 CN;

Query Match 98.6%; Score 1378; DB 2; Length 193;
Best Local Similarity 97.4%; Pred. No. 1.90e-113;
Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|||:|||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    181 GALVTVGAFFASK 193
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RESULT 5
ID US-08-978-523-6 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08978523
XX
CC Sequence 6, Application US/08978523
CC Patent No. 5883229
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/978,523
CC FILING DATE: herewith
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140002
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 192 AA; 20701 MW; 181510 CN;

Query Match 97.9%; Score 1368; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.58e-112;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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  Query Match           98.7%;  Score 1379;  DB 1;  Length 193;
  Best Local Similarity  98.4%;  Pred. No. 1.54e-113;
  Matches   190;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db     181 GALVTVGAFFASK 193
           |||||||||||||
Qy     181 GALVTVGAFFASK 193


RESULT    2
ID   US-08-978-523-4     STANDARD;     PRT;   193 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 4, Application US/08978523
XX
CC    Sequence 4, Application US/08978523
CC    Patent No. 5883229
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/978,523
CC         FILING DATE:  herewith
CC         CLASSIFICATION:  424
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140002
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20832 MW; 183365 CN;

  Query Match           98.7%;  Score 1379;  DB 2;  Length 193;
  Best Local Similarity  98.4%;  Pred. No. 1.54e-113;
  Matches   190;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db       1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Db     181 GALVTVGAFFASK 193
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Qy     181 GALVTVGAFFASK 193


RESULT    3
ID   US-08-798-897-3     STANDARD;     PRT;   193 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 3, Application US/08798897
XX
CC    Sequence 3, Application US/08798897
CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20820 MW; 185063 CN;

  Query Match           98.6%;  Score 1378;  DB 1;  Length 193;
  Best Local Similarity  97.4%;  Pred. No. 1.90e-113;
  Matches   188;  Conservative    4;  Mismatches   1;  Indels   0;  Gaps   0;
```

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:16:05 2000; MasPar time 5.04 Seconds
552.912 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-7
Description: (1-193) from US09155327B.pep
Perfect Score: 1397
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 30.708; Variance 142.172; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1379	98.7	193	1	US-08-798-	Sequence 4, Applicatio	1.54e-113
2	1379	98.7	193	2	US-08-978-	Sequence 4, Applicatio	1.54e-113
3	1378	98.6	193	1	US-08-798-	Sequence 3, Applicatio	1.90e-113
4	1378	98.6	193	2	US-08-978-	Sequence 3, Applicatio	1.90e-113
5	1368	97.9	192	2	US-08-978-	Sequence 6, Applicatio	1.58e-112
6	1368	97.9	192	1	US-08-798-	Sequence 6, Applicatio	1.58e-112
7	1367	97.9	192	2	US-08-978-	Sequence 5, Applicatio	1.95e-112
8	1367	97.9	192	1	US-08-798-	Sequence 5, Applicatio	1.95e-112
9	616	44.1	233	4	PCT-US95-0	Sequence 24, Applicati	6.27e-44
10	616	44.1	233	4	PCT-US94-0	Sequence 7, Applicatio	6.27e-44
11	616	44.1	233	2	US-08-470-	Sequence 7, Applicatio	6.27e-44
12	616	44.1	233	3	US-08-471-	Sequence 14, Applicati	6.27e-44
13	616	44.1	233	1	US-08-333-	Sequence 59, Applicati	6.27e-44
14	616	44.1	233	1	US-08-081-	Sequence 6, Applicatio	6.27e-44
15	616	44.1	233	2	US-08-661-	Sequence 59, Applicati	6.27e-44
16	616	44.1	233	1	US-08-471-	Sequence 14, Applicati	6.27e-44
17	616	44.1	233	1	US-08-607-	Sequence 24, Applicati	6.27e-44
18	587	42.0	233	1	US-08-607-	Sequence 23, Applicati	2.51e-41
19	587	42.0	233	4	PCT-US95-0	Sequence 23, Applicati	2.51e-41
20	586	41.9	239	2	US-08-337-	Sequence 10, Applicati	3.09e-41
21	586	41.9	239	2	US-08-856-	Sequence 10, Applicati	3.09e-41
22	586	41.9	239	1	US-08-248-	Sequence 10, Applicati	3.09e-41
23	586	41.9	239	2	US-08-856-	Sequence 10, Applicati	3.09e-41
24	586	41.9	239	1	US-08-112-	Sequence 10, Applicati	3.09e-41
25	584	41.8	236	1	US-08-607-	Sequence 22, Applicati	4.67e-41
26	584	41.8	236	4	PCT-US95-0	Sequence 22, Applicati	4.67e-41
27	581	41.6	239	1	US-08-607-	Sequence 20, Applicati	8.68e-41
28	581	41.6	239	3	US-08-471-	Sequence 12, Applicati	8.68e-41
29	581	41.6	239	4	PCT-US95-0	Sequence 20, Applicati	8.68e-41
30	581	41.6	239	1	US-08-471-	Sequence 12, Applicati	8.68e-41
31	579	41.4	236	1	US-08-607-	Sequence 21, Applicati	1.31e-40
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33	575	41.2	239	1	US-08-690-	Sequence 4, Applicatio	2.99e-40
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36	575	41.2	239	1	US-08-248-	Sequence 12, Applicati	2.99e-40
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39	575	41.2	239	5	5459251-2	atent No. 5459251	2.99e-40
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ALIGNMENTS

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ID   US-08-798-897-4     STANDARD;     PRT;   193 AA.
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XX
DT
XX
DE   Sequence 4, Application US/08798897
XX
CC    Sequence 4, Application US/08798897
CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20832 MW; 183365 CN;
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  Matches  204;  Conservative    0;  Mismatches  138;  Indels    1;  Gaps    1;

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           || ||||||| |    |||| |   |      | | |||| | || | ||    || ||
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Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | ||||||| |||| | ||  || ||   ||||| ||| ||
Db     411 GACGACTTCTCCCGCCGCTACCGCCGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 352

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  |||||| ||  |||    || || || |||   |  ||
Db     351 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 292

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
           ||||||||  |  ||||||| ||||||| || || |  | | ||||||  |||||
Db     291 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 232

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
           ||||||   || |||  |||  ||||||   |  ||      |||||    |  ||||||
Db     231 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 172

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctggg 433
           |    |  |||     |||||||||    |  || |||||||
Db     171 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGG 129


RESULT  15
AA939725/c
LOCUS       AA939725      515 bp    mRNA            EST       01-MAY-1998
DEFINITION  vz92a11.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1344668 5' similar to gb:L31532_rna1 Mouse bcl-2 gene
            encoding mbcl-2-beta (MOUSE);, mRNA sequence.
ACCESSION   AA939725
VERSION     AA939725.1  GI:3099269
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2285479.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:693460
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 304.
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1344668"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      125 a    168 c    130 g     92 t
ORIGIN


  Query Match             18.3%;  Score 106.6;  DB 40;  Length 515;
  Best Local Similarity   60.6%;  Pred. No. 4.6e-17;
  Matches  175;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy     145 gctggagacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagcta 204
           ||||| || || ||       || | ||| ||   |||| | ||  || ||  ||||||
Db     421 GCTGGGGATGACTTCTCTCGTCGCTACCGTCGTGACTTCGCAGAGATGTCCAGTCAGCTG 362

Qy     205 cacgtgaccccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaa 264
           ||| |||| ||   | | ||   |  ||||||  ||  |||    || ||||| |||
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Qy     265 gggggccctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgct 324
           |  ||    |||||||  |  ||||||| |||||||  || || |  | | ||||||
Db     301 GATGGGGTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTG 242

Qy     325 gagagtgtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcc 384
           ||||| |||||||  || |||   ||  ||||||   |  ||      |||||    |
Db     241 GAGAGCGTCAACAGGGAGATGTCACCCCTGGTGGACAACATCGCCCTGTGGATGACTGAG 182

Qy     385 tacctggagacacgtctggctgactggatccacagcagtggcggctggg 433
           ||||||  |    | ||||     |||||||||    |  || |||||||
Db     181 TACCTGAACCGGCATCTGCACACCTGGATCCAGGATAACGGAGGCTGGG 133


Search completed: July  4, 2000, 01:06:10
Job time: 16529 sec
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  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     On Jul 7, 1999 this sequence version replaced gi:5866278.
            Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means is determined.
            Seq primer: M13 Forward
            POLYA=No.
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                     /strain="C57BL/6J"
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                     /clone="UI-M-BH2.1-apn-b-04-0-UI"
                     /clone_lib="NIH_BMAP_M_S3.1"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S3.1 library is a subtracted library of a
                     series, ultimately derived from a mixture of individually
                     tagged normalized libraries from ten regions of the mouse
                     brain (cerebellum, brain stems, olfactory bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland, striatum, hipoccampus) after a series of
                     subtractions to reduce the representation of cDNAs from
                     which ESTs had already been generated. The following
                     serially subtracted libraries were generated in this
                     process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
                     The subtracted library (NIH_BMAP_M_S3.1) was constructed
                     as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
                     clones from which 3' ESTs had been derived was used as a
                     driver in a hybridization with the NIH_BMAP_M_S2 library
                     in the form of single-stranded circles. The remaining
                     single-stranded circles (subtracted library) was purified
                     by hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (LifeTechnologies) to generate the
                     NIH_BMAP_M_S3.1 library. This procedure has been
                     previously described (Bonaldo, Lennon and Soares, Genome
                     Research 6:791-806, 1996)
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                     TAG_TISSUE=hippocampus
                     TAG_SEQ=TCAAG"
BASE COUNT       86 a    147 c    111 g    110 t
ORIGIN


  Query Match             19.0%;  Score 110.2;  DB 69;  Length 454;
  Best Local Similarity   58.3%;  Pred. No. 5.5e-18;
  Matches  193;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy     101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
           |||| |      ||   |   |  || | |||||  || | |  || || || |||||||
Db     331 GGGAGGTGATTCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCAGGCGATGAGTTTG 272

Qy     161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
           |    || | |||  |  | |||  ||| ||  |  | |||||  ||| | ||||||||
Db     271 AACTGCGGTACCGGAGAGCGTTCAGTGATCTAACATCCCAGCTTCACATAACCCCAGGGA 212

Qy     221 cagcccagcaacgcttcacccaggtttccgacgaacttttccaaggggccctaactggg 280
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           | ||  | ||  ||||    |||||     | ||||| || |  |  ||    |||||||
Db     211 CCGCGTATCAGAGCTTTGAGCAGGTAGTGAATGAACTCTTTCGGGATGGAGTAAACTGGG 152

Qy     281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
           | ||  | ||||| || ||   |||||| |  || ||||| |  || || ||  |||| |
Db     151 GTCGCATCGTGGCCTTTTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 92

Qy     341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
           | ||| ||   |||||| | |   |      ||||||  |   |||| ||| |    | |
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Qy     401 tggctgactggatccacagcagtggcggctg 431
           | |     ||||||||    |  |||||| |
Db      31 TAGAGCCTTGGATCCAGGAGAACGGCGGCCG 1


RESULT  14
AI401297/c
LOCUS       AI401297      471 bp    mRNA            EST       30-MAR-1999
DEFINITION  tg92c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116234 3'
            similar to gb:M13995 PROTEIN BCL-2-BETA (HUMAN);contains TAR1.t2
            MER22 repetitive element ;, mRNA sequence.
ACCESSION   AI401297
VERSION     AI401297.1  GI:4244384
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Apr 7, 1998 this sequence version replaced gi:3035272.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Insert Length: 2629   Std Error: 0.00
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            High quality sequence stop: 445.
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     source          1. .471
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                     /clone="IMAGE:2116234"
                     /clone_lib="NCI_CGAP_CLL1"
                     /tissue_type="B-cell, chronic lymphotic leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       91 a    173 c    130 g     77 t
ORIGIN


  Query Match             19.0%;  Score 110.2;  DB 46;  Length 471;
  Best Local Similarity   59.5%;  Pred. No. 5.6e-18;
```

UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_LIB=UI-R-Y0
TAG_TISSUE=Eye
TAG_SEQ=CATTG"

BASE COUNT 88 a 128 c 92 g 96 t
ORIGIN

Query Match 20.0%; Score 116.2; DB 51; Length 404;
Best Local Similarity 59.6%; Pred. No. 1.6e-19;
Matches 196; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

```
Qy    101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
          |||| |      ||   |   |  || | |||||  || | |  ||||| || ||||||||
Db    383 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 324

Qy    161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
          |    || | |||  |  | |||  ||| ||  |  | ||||| ||  | ||||||||
Db    323 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 264

Qy    221 cagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggccctaactggg 280
          ||||  | ||  ||||    |||||     | ||||| || |  |  ||    |||||||
Db    263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 204

Qy    281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
          | ||  ||||||| ||||   |||||| |  || ||||| |  || || ||  |||| |
Db    203 GTCGCATTGTGGCCTTCTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 144

Qy    341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
          | ||| ||   |||||| | |   |      |||||| |  |||||||| |    |  |
Db    143 AGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGCCACCTACCTGAATGACCACC 84

Qy    401 tggctgactggatccacagcagtggcggc 429
          | |    ||||||||    |  ||||||
Db     83 TAGAGCCTTGGATCCAGGAGAACGGCGGC 55
```

RESULT 12
F08773
LOCUS F08773 299 bp mRNA EST 20-FEB-1995
DEFINITION HSC25B061 normalized infant brain cDNA Homo sapiens cDNA clone c-25b06, mRNA sequence.
ACCESSION F08773
VERSION F08773.1 GI:673075
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534

COMMENT On Sep 21, 1992 this sequence version replaced gi:276079.
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-25b06
Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 339.
FEATURES Location/Qualifiers
source 1. .299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-25b06"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
BASE COUNT 67 a 69 c 94 g 67 t 2 others
ORIGIN

Query Match 19.7%; Score 114.4; DB 21; Length 299;
Best Local Similarity 62.2%; Pred. No. 4.2e-19;
Matches 178; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

```
Qy    148 ggagacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacac 207
          || |||||||||||    || | ||| ||  | |||  |||||||  |  | ||||| |||
Db      1 GGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCAC 60

Qy    208 gtgaccccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaaggg 267
           | ||||||||  ||||  | ||  ||||    |||||     | ||||| ||||  |
Db     61 ATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGAT 120

Qy    268 ggccctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgag 327
          ||    |||||||| ||  ||||||| || ||   ||| || |  || ||||  |  ||
Db    121 GGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTNCGTGGAA 180

Qy    328 agtgtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctac 387
          || ||  |||| || ||| ||   |||||| |     ||   | || ||| |   | |||
Db    181 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTNGGATCGCAGCTTAGATGGCCACTTAC 240

Qy    388 ctggagacacgtctggctgactggatccacagcagtggcggctggg 433
          ||| |    |  || |     ||||||||    |  ||||||||||
Db    241 CTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 286
```

RESULT 13
AW124015/c
LOCUS AW124015 454 bp mRNA EST 22-OCT-1999
DEFINITION UI-M-BH2.1-apn-b-04-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone UI-M-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
ACCESSION AW124015
VERSION AW124015.1 GI:6099545
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 454)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

```
Qy    113 ccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttcc 172
          || | |   |  |  | |||||  || |||  || || ||||||||||    || | ||
Db      1 CCACNGGAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACC 60

Qy    173 gccgcaccttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaac 232
          | ||  | |||  ||||||| |  | ||||| ||| | ||||||||  ||||  | ||
Db     61 GGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGA 120

Qy    233 gcttcacccaggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtgg 292
          ||||    |||||     | ||||| ||||  |  ||    |||||||| ||  ||||||
Db    121 GCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGG 180

Qy    293 cattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctt 352
          | || ||   ||| || |  || ||||| |  || || ||  |||| || ||| ||   |
Db    181 CCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTAT 240

Qy    353 tggtgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgac-tgg 411
          ||||| | |   ||   | |||||| |   | ||||||    |  || |  | | |||
Db    241 TGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAAGCCTTGG 300

Qy    412 atccacagcagtggcggctggg 433
          |||||    |  ||||||||||
Db    301 ATCCAGGAGAACGGCGGCTGGG 322
```

RESULT 10
AL134785

LOCUS	AL134785 584 bp mRNA EST 29-DEC-1999
DEFINITION	DKFZp547K2090_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547K2090 5', mRNA sequence.
ACCESSION	AL134785
VERSION	AL134785.1 GI:6602972
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 584)
AUTHORS	Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE	EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL	Unpublished (1999)
COMMENT	On Jul 7, 1999 this sequence version replaced gi:5866255. Contact: Poustka A.J. Department Lehrach Max-Planck-Institute for Molecular Genetics Ihnestrasse 73, 14195 Berlin, Germany Tel: +49-30-84131623 Fax: +49-30-84131128 Email: poustka@mpimg-berlin-dahlem.mpg.de This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available. This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES	Location/Qualifiers
source	1. .584
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="DKFZp547K2090"
	/clone_lib="547 (synonym: hfbr1)"
	/tissue_type="brain"
	/dev_stage="fetal"
	/lab_host="Xl-2blue"
	/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

BASE COUNT 144 a 145 c 173 g 116 t 6 others
ORIGIN

```
  Query Match             20.3%;  Score 118.2;  DB 79;  Length 584;
  Best Local Similarity   62.3%;  Pred. No. 5.8e-20;
  Matches  180;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db    293 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 352

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          ||||| |  | ||||| ||| | ||||||||  ||||  | ||  ||||    |||||
Db    353 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCANAGCTTTGAACAGGTAG 412

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  ||||||| || ||   ||| |
Db    413 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 472

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || ||||| |  || || ||  |||| || ||| |    |||||| | |  |  |
Db    473 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCANGTATTGGTGAGTCCNGATC 532

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatcca 416
            |||||| |   | |||||| |     |  ||       ||||||||
Db    533 GCACTTGGATGGCCACTTACCTGAATGACCACCTANANNCTTGGATCCA 581
```

RESULT 11
AI716839/c

LOCUS	AI716839 404 bp mRNA EST 10-JUN-1999
DEFINITION	UI-R-Y0-acg-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
ACCESSION	AI716839
VERSION	AI716839.1 GI:5034095
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 404)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	On May 18, 1998 this sequence version replaced gi:3136946. Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA=No.

FEATURES	Location/Qualifiers
source	1. .404
	/organism="Rattus norvegicus"
	/strain="Sprague-Dawley"
	/db_xref="taxon:10116"
	/clone="UI-R-Y0-acg-g-07-0-UI"
	/clone_lib="UI-R-Y0"
	/dev_stage="adult"
	/lab_host="DH10B (Life Technologies)"
	/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,

```
  Query Match             23.3%;  Score 135.6;  DB 109;  Length 549;
  Best Local Similarity   94.0%;  Pred. No. 2.4e-24;
  Matches  141;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
          |||||| |||||||||||||||||||||||| |||||||||| || ||||||||||||||
Db    261 GGCGGAGTTCACAGCTCTATACGGGGACGGAGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 320

Qy    492 gggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactgggggccctggt 551
          ||| |||||||||| |||||| |||||| ||||||||||||||||||||||||||||||
Db    321 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 380

Qy    552 aactgtaggggccttttttgctagcaagtg 581
          |||||||||||||| ||||||||||||||
Db    381 AACTGTAGGGGCCTTGTTTGCTAGCAAGTG 410


RESULT   8
AQ401160
LOCUS       AQ401160      455 bp    DNA              GSS       13-MAR-1999
DEFINITION  HS_5062_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
ACCESSION   AQ401160
VERSION     AQ401160.1  GI:4412503
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 638  row: M  column: 4
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 455.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=638 Col=4 Row=M"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT       80 a    111 c    142 g    117 t      5 others
ORIGIN


  Query Match             21.3%;  Score 124;  DB 106;  Length 455;
  Best Local Similarity   88.7%;  Pred. No. 1.9e-21;
  Matches  133;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy    432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
          |||||| |||||||||||||||||||||||| |||||||||| || ||||||||||||||
Db    224 GGCGGAGTTCACAGCTCTATACGGTGACAGCGCCCTGGAGGATGCGCGGCGTCTGCGGGA 283

Qy    492 gggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactgggggccctggt 551
          ||| |||||||||| |||||| |||||| |||| | |||||||||||| |||||||| ||
Db    284 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACNGTGGCCGTGGCACTTGGGGCCCTTGT 343

Qy    552 aactgtaggggccttttttgctagcaagtg 581
          ||||||| ||||||||||  |||||||||
Db    344 AACTGTANGGGCCTTTTTTTGTAGCAAGTG 373


RESULT   9
W01420
LOCUS       W01420        437 bp    mRNA             EST       18-APR-1996
DEFINITION  za73d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
            BCL-X. ;, mRNA sequence.
ACCESSION   W01420
VERSION     W01420.1  GI:1273428
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785898.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 383.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Homo sapiens"
                     /db_xref="GDB:1243109"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:298187"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT       99 a    106 c    140 g     89 t      3 others
ORIGIN


  Query Match             20.7%;  Score 120.2;  DB 25;  Length 437;
  Best Local Similarity   62.7%;  Pred. No. 1.7e-20;
  Matches  202;  Conservative    0;  Mismatches  119;  Indels    1;  Gaps    1;
```

cDNA synthesis with oligo dT Xba I (Xba I cloning site).
RNA: stage 50-56 tadpoles, total brain tissue, GTC
extraction method."
BASE COUNT 108 a 70 c 118 g 120 t
ORIGIN

Query Match 25.8%; Score 150; DB 71; Length 416;
Best Local Similarity 70.3%; Pred. No. 5.2e-28;
Matches 201; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```
Qy    296 tctttgtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttgg 355
          | ||| | ||||| || || ||||||||||||||||||||||| || |||   ||| |
Db      5 TTTTTTTTTTTTGGTGCCGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGTCCCCTCTTC 64

Qy    356 tgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgactggatcc 415
          ||  ||   | || || ||||| ||| | || ||||||||||   |||   | ||||||
Db     65 TGCCACGGATTCAAGACTGGATGGTGACATATCTGGAGACAAACCTGAGAGGCTGGATTC 124

Qy    416 acagcagtggcggctgggcggacttcacagctctatacggggacggggccctggaggacg 475
          | |||| |||  |||||   |  ||   | ||||||| ||||| || ||| | || || |
Db    125 AGAGCAATGGATGCTGGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAG 184

Qy    476 cacggcgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtgg 535
          |  || | |  || ||||| || ||||||| | |||  || ||  | || || || || |
Db    185 CCAGGAGGCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAACTGGAGCGGTAG 244

Qy    536 cactgggggccctggtaactgtaggggccttttttgctagcaagtg 581
          | ||||| ||  || | || ||||| ||||| ||||| ||||||||
Db    245 CTCTGGGTGCTTTGATGACAGTAGGAGCCTTGTTTGCCAGCAAGTG 290
```

RESULT 6
AQ532175
LOCUS AQ532175 628 bp DNA GSS 18-MAY-1999
DEFINITION RPCI-11-352L5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-352L5, genomic survey sequence.
ACCESSION AQ532175
VERSION AQ532175.1 GI:4844050
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 628)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT On Feb 19, 1999 this sequence version replaced gi:4145213.
Other_GSSs: RPCI-11-352L5.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .628
/organism="Homo sapiens"
/db_xref="GDB:7635052"
/db_xref="taxon:9606"
/clone="RPCI-11-352L5"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 128 a 130 c 237 g 133 t
ORIGIN

Query Match 23.9%; Score 138.8; DB 108; Length 628;
Best Local Similarity 95.3%; Pred. No. 3.9e-25;
Matches 143; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy    432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
          |||||| ||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db    233 GGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGA 292

Qy    492 gggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactgggggccctggt 551
          ||| |||||||||| |||||| |||||| ||||||||||||||||||||||||||||||
Db    293 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 352

Qy    552 aactgtaggggccttttttgctagcaagtg 581
          ||||||||||||||||||||||||||||||
Db    353 AACTGTAGGGGCCTTTTTTGCTAGCAAGTG 382
```

RESULT 7
AQ665088
LOCUS AQ665088 549 bp DNA GSS 23-JUN-1999
DEFINITION HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
ACCESSION AQ665088
VERSION AQ665088.1 GI:5172856
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 916 row: B column: 11
Seq primer: T7
Class: BAC ends
High quality sequence stop: 549.
FEATURES Location/Qualifiers
source 1. .549
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=916 Col=11 Row=B"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT 105 a 126 c 190 g 118 t 10 others
ORIGIN

```
Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
           | ||||||||||||||| ||||| |||||||||| || ||||| |||||||| || |||
Db     214 AAGCTGAGGCAGAAGGGGTATGTTTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 273

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
           ||||| |||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db     274 CCGCTACACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 333

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
           |||||| || ||||| |||||||| || |||||||| ||||| ||||||||||||||||||
Db     334 TTCTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC 393

Qy     241 caggtttccgacgaacttttccaaggggggccctaactggg 280
           ||||| || || ||||| |||||||||||||| |||||||
Db     394 CAGGTCTCTGATGAACTCTTCCAAGGGGGCCCCAACTGGG 433
```

RESULT 4
AW048567/c
LOCUS AW048567 431 bp mRNA EST 18-SEP-1999
DEFINITION UI-M-BH1-alx-e-10-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alx-e-10-0-UI 3', mRNA sequence.
ACCESSION AW048567
VERSION AW048567.1 GI:5909096
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 431)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Feb 18, 1999 this sequence version replaced gi:4297581.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .431
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH1-alx-e-10-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.
TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=corpus-striatum
TAG_SEQ=ACGGC"
BASE COUNT 105 a 131 c 85 g 110 t
ORIGIN

```
  Query Match             30.8%;  Score 179.2;  DB 64;  Length 431;
  Best Local Similarity   98.4%;  Pred. No. 2.4e-35;
  Matches  181;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     250 gacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttggg 309
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 GACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGG 372

Qy     310 gctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtccag 369
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     371 GCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTGCAG 312

Qy     370 gattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcggc 429
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     311 GATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGGC 252

Qy     430 tggg 433
           ||||
Db     251 TGGG 248
```

RESULT 5
AW159063
LOCUS AW159063 416 bp mRNA EST 05-NOV-1999
DEFINITION za50h02.x1 Xenopus EST library Xenopus laevis cDNA clone za50h02 5', mRNA sequence.
ACCESSION AW159063
VERSION AW159063.1 GI:6271092
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 416)
AUTHORS Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,R., Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and McCombie,W.R.
TITLE Expressed sequence tags from Xenopus
JOURNAL Unpublished (1999)
COMMENT On Jun 5, 1998 this sequence version replaced gi:3189433.
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.
FEATURES Location/Qualifiers
source 1. .416
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="za50h02"
/clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
/cell_line="W22-TGA"
/dev_stage="tadpole"
/note="Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs).

```
Db    531 AGTGGGGGCT 540


RESULT   2
AA596919
LOCUS       AA596919      362 bp    mRNA            EST       19-SEP-1997
DEFINITION  vo21f08.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
            IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
            sequence.
ACCESSION   AA596919
VERSION     AA596919.1  GI:2412354
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 362)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Dec 18, 1996 this sequence version replaced gi:1734345.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:582143
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 334.
FEATURES             Location/Qualifiers
     source          1. .362
                     /organism="Mus musculus"
                     /strain="C3H"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1050567"
                     /clone_lib="Barstead mouse myotubes MPLRB5"
                     /cell_line="C2C12"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [AATTCGGATCCTTG], digested with Not I and cloned into the
                     Not I  and Eco RI sites of the modified pT7T3 vector.
                     Library constructed  by Bob Barstead.  The C2C12 cell line
                     (available from ATCC,  catalog # CRL-1772) differentiates
                     rapidly, forming contractile  myotubes and producing
                     characteristic muscle proteins.   "
BASE COUNT       64 a    116 c    107 g     75 t
ORIGIN


  Query Match           55.4%;  Score 321.8;  DB 35;  Length 362;
  Best Local Similarity  97.9%;  Pred. No. 3e-71;
  Matches  326;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      6 gaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctataggct 65
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Db     29 GACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATAAGCT 88

Qy     66 gaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgacccgct 125
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     89 GAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACCCGCT 148

Qy    126 gcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctc 185
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    149 GCACCAAGCCATGCGTGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTC 208

Qy    186 tgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggt 245
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 TGAACTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGT 268

Qy    246 ttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctt 305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 TTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTT 328

Qy    306 tggggctgccctgtgtgctgagagtgtcaacaa 338
          |||||||||||||||||||||||||||||  ||
Db    329 TGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAA 361


RESULT   3
AW326901
LOCUS       AW326901      433 bp    mRNA            EST       27-JAN-2000
DEFINITION  20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW326901
VERSION     AW326901.1  GI:6762822
KEYWORDS    EST.
SOURCE      Bos taurus.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
            Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1133576.
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 10  row: G  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT       80 a    142 c    143 g     68 t
ORIGIN


  Query Match           39.4%;  Score 228.8;  DB 80;  Length 433;
  Best Local Similarity  88.6%;  Pred. No. 8e-48;
  Matches  248;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| |||||||||||||  |||||||||||||| |||||||||| |||||||| ||||||
Db    154 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTAGTGGCAGACTTTGTGGGCTAT 213
```

	No.	Score	Match	Length	DB	ID	Description
	1	403.6	69.5	540	79	AW258810	AW258810 um74a02.y
	2	321.8	55.4	362	35	AA596919	AA596919 vo21f08.r
	3	228.8	39.4	433	80	AW326901	AW326901 20104 MAR
c	4	179.2	30.8	431	64	AW048567	AW048567 UI-M-BH1-
	5	150	25.8	416	71	AW159063	AW159063 za50h02.x
	6	138.8	23.9	628	108	AQ532175	AQ532175 RPCI-11-3
	7	135.6	23.3	549	109	AQ665088	AQ665088 HS_5340_B
	8	124	21.3	455	106	AQ401160	AQ401160 HS_5062_A
	9	120.2	20.7	437	25	W01420	W01420 za73d06.r1
	10	118.2	20.3	584	79	AL134785	AL134785 DKFZp547K
c	11	116.2	20.0	404	51	AI716839	AI716839 UI-R-Y0-a
	12	114.4	19.7	299	21	F08773	F08773 HSC25B061 n
c	13	110.2	19.0	454	69	AW124015	AW124015 UI-M-BH2.
c	14	110.2	19.0	471	46	AI401297	AI401297 tg92c06.x
c	15	106.6	18.3	515	40	AA939725	AA939725 vz92a11.r
	16	104	17.9	472	43	AI180733	AI180733 ub91d09.r
c	17	96.6	16.6	471	34	AA509753	AA509753 vh52c06.r
	18	70.2	12.1	1696	83	AF149300	AF149300 Rattus no
c	19	57.4	9.9	574	81	AW418903	AW418903 ha15d05.x
	20	57	9.8	516	22	H09884	H09884 ym05b07.r1
	21	46.6	8.0	616	44	AI323048	AI323048 mj41h10.y
	22	44.4	7.6	278	60	AV138827	AV138827 AV138827
	23	44.2	7.6	478	61	AI837675	AI837675 UI-M-AK0-
c	24	44.2	7.6	497	27	AA016399	AA016399 mg88g02.r
	25	44.2	7.6	540	44	AI326919	AI326919 mj39b01.x
	26	44.2	7.6	592	27	AA051441	AA051441 mj41h10.r
	27	44.2	7.6	616	26	W97433	W97433 mf95f12.r1
	28	42.8	7.4	640	40	AA981864	AA981864 ua36g07.r
c	29	42.6	7.3	547	41	AI020744	AI020744 ub01h12.r
c	30	42.2	7.3	418	34	AA458294	AA458294 vg48c03.r
c	31	42.2	7.3	747	74	AW226585	AW226585 up09f12.x
c	32	41.8	7.2	925	82	CNS0091P	AL053013 Drosophil
c	33	41.6	7.2	534	44	AI322704	AI322704 mj39b01.y
c	34	41.6	7.2	545	26	W42014	W42014 mb16g04.r1
	35	41.4	7.1	925	82	CNS0091P	AL053013 Drosophil
c	36	41.2	7.1	446	27	AA049970	AA049970 mj39b01.r
c	37	40.8	7.0	1201	83	CNS016BR	AL106545 Drosophil
c	38	40.6	7.0	714	64	AW072826	AW072826 xa42e07.x
	39	40	6.9	274	20	T29044	T29044 EST66242 Hu
c	40	40	6.9	377	80	AW355100	AW355100 37259 MAR
c	41	39.6	6.8	624	44	AI323521	AI323521 mo57b02.x
	42	39.4	6.8	835	49	AI656482	AI656482 tt51c06.x
c	43	38.8	6.7	939	82	CNS00CNG	AL059400 Drosophil
c	44	38.2	6.6	844	82	CNS0052P	AL056652 Drosophil
	45	37.4	6.4	521	48	AI599840	AI599840 EST251543

ALIGNMENTS

```
RESULT   1
AW258810
LOCUS       AW258810       540 bp    mRNA            EST       23-DEC-1999
DEFINITION  um74a02.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
            IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
            REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
ACCESSION   AW258810
VERSION     AW258810.1  GI:6631791
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     On May 18, 1998 this sequence version replaced gi:3137956.
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1009678
            Seq primer: custom primer used
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
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                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2300906"
                     /clone_lib="Sugano mouse kidney mkia"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
BASE COUNT       98 a    165 c    170 g    107 t
ORIGIN


  Query Match             69.5%;  Score 403.6;  DB 79;  Length 540;
  Best Local Similarity   97.7%;  Pred. No. 9.3e-92;
  Matches  420;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

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Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
           | |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     172 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 231

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db     232 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 291

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 351

Qy     241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db     472 CAAGTGCATGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGAT-CACAGC 530

Qy     421 agtggcggct 430
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2000, 01:06:08 ; Search time 795.04 Seconds
(without alignments)
2962.018 Million cell updates/sec

Title: US-09-155-327B-8
Perfect score: 581
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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109: gb_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

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Db   2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy    451 tacgg 455
          |||||
Db   2062 TACGG 2066


RESULT  14
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; Sequence 4, Application PC/TUS9305651
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  A Gene Which Prevents Programmed Cell Death
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  diskette
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/05651
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1459..2178
;      OTHER INFORMATION:  /product= "Bcl-2"
PCT-US93-05651-4


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Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
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Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
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Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
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Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

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Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
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Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
          |||||
Db    2062 TACGG 2066


RESULT  15
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; Sequence 2, Application PC/TUS9306251
;  GENERAL INFORMATION:
;    APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;    TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;    TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06251
;      FILING DATE:  19930630
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-2


  Query Match             21.5%;  Score 125;  DB 6;  Length 5086;
  Best Local Similarity   58.9%;  Pred. No. 3.7e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

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Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || |||   |  ||
Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
           |||||||| |  ||||||| |||||||  || || |  | | ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
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Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
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Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
          |||||
Db    2062 TACGG 2066


Search completed: July  4, 2000, 01:24:30
Job time: 14818 sec
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;       COUNTRY:  USA
;       ZIP:  94306
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/365,486A
;       FILING DATE:  23-DEC-1994
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sholtz, Charles K.
;       REGISTRATION NUMBER:  38,615
;       REFERENCE/DOCKET NUMBER:  8255-0018
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 324-0880
;       TELEFAX:  (415) 324-0960
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5086 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  human bcl-2 cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1459..2178
US-08-365-486A-14


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  Best Local Similarity   58.9%;  Pred. No. 3.7e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy      91 gctgggcctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
           || ||||||| |    |||| |   |       | | ||||  ||| | ||    || ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | |||| ||  |||| | ||  || ||   ||||| ||| ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
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Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
           |||||||| |  ||||||| |||||||  || || |  | | ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
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Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
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Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
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Db    2062 TACGG 2066


RESULT  13
US-09-080-285-19
; Sequence 19, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;     APPLICANT:  Reed, John
;     TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;     NUMBER OF SEQUENCES:  29
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;       ADDRESSEE:  P.C.
;       STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;       CITY:  Arlington
;       STATE:  Virginia
;       COUNTRY:  U.S.A.
;       ZIP:  22202
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/080,285
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/465,485
;       FILING DATE:  05-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/124,256
;       FILING DATE:  20-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/840,716
;       FILING DATE:  21-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/288,692
;       FILING DATE:  22-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fortney, Andrew D.
;       REGISTRATION NUMBER:  34,600
;       REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (408) 436-2070
;       TELEFAX:  (408) 436-2075
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5086 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-080-285-19


  Query Match             21.5%;  Score 125;  DB 5;  Length 5086;
  Best Local Similarity   58.9%;  Pred. No. 3.7e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy      91 gctgggcctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
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Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
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Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
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Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
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Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/228,704
;      FILING DATE: 18-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 994,941
;      FILING DATE: 23-DEC-1992
;      APPLICATION NUMBER: 663,010
;      FILING DATE: 19-MAR-1991
;      APPLICATION NUMBER: 883,687
;      FILING DATE: 09-JUL-1986
;SEQ ID NO:1:
;      LENGTH: 4825
5459251-1


  Query Match             21.5%;  Score 125;  DB 7;  Length 4825;
  Best Local Similarity   58.9%;  Pred. No. 3.7e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

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           || ||||||| |    |||| |    |      | | ||||  ||| | ||    || ||
Db    1702 gcggggcctgcgctcagcccggtgccacctgtggtccacctggccctccgccaagccggc 1761

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | |||| ||  |||| | ||  || ||   ||||| ||| ||
Db    1762 gacgacttctcccgccgctaccgcggcgacttcgccgagatgtccagccagctgcacctg 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || |||   |  ||
Db    1822 acgcccttcaccgcgcggggacgctttgccacggtggtggaggagctcttcagggacggg 1881

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
              ||||||||  |  ||||||| |||||||  || || |  | | ||||||  |||||
Db    1882 gtgaactgggggaggattgtggccttctttgagttcggtggggtcatgtgtgtggagagc 1941

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
           ||||||   || |||  |||  ||||||   |  ||      |||||    |  ||||||
Db    1942 gtcaaccgggagatgtcgcccctggtggacaacatcgccctgtggatgactgagtacctg 2001

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
             |    | |||     |||||||||    | || |||||||  | |||    |  ||
Db    2002 aaccggcacctgcacacctggatccaggataacggaggctgggatgcctttgtggaactg 2061

Qy     451 tacgg 455
           |||||
Db    2062 tacgg 2066


RESULT  11
US-08-465-485A-19
; Sequence 19, Application US/08465485A
; Patent No. 5831066
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,485A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5086 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-465-485A-19


  Query Match             21.5%;  Score 125;  DB 3;  Length 5086;
  Best Local Similarity   58.9%;  Pred. No. 3.7e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy      91 gctgggcctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
           || ||||||| |    |||| |    |      | | ||||  ||| | ||    || ||
Db    1702 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 1761

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | |||| ||  |||| | ||  || ||   ||||| ||| ||
Db    1762 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 1821

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || |||   |  ||
Db    1822 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 1881

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
              ||||||||  |  ||||||| |||||||  || || |  | | ||||||  |||||
Db    1882 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 1941

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
           ||||||   || |||  |||  ||||||   |  ||      |||||    |  ||||||
Db    1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
             |    | |||     |||||||||    | || |||||||  | |||    |  ||
Db    2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061

Qy     451 tacgg 455
           |||||
Db    2062 TACGG 2066


RESULT  12
US-08-365-486A-14
; Sequence 14, Application US/08365486A
; Patent No. 5834306
;  GENERAL INFORMATION:
;    APPLICANT:  Webster, Keith A.
;    APPLICANT:  Bishopric, Nanette H.
;    TITLE OF INVENTION:  Tissue Specific Hypoxia Regulated
;    TITLE OF INVENTION:  Therapeutic Constructs
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..717
US-08-465-485A-20
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  Query Match             21.5%;  Score 125;  DB 3;  Length 717;
  Best Local Similarity   58.9%;  Pred. No. 1.8e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy      91 gctgggcctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
           || ||||||| |    |||| |   |       | | ||||  ||| | ||    || ||
Db     244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | |||| ||  |||| | ||  || ||   ||||| ||| ||
Db     304 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 363

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || |||   |  ||
Db     364 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 423

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
           ||||||||  |  ||||||| |||||||  || || |  | | ||||||  |||||
Db     424 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 483

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
           ||||||   || |||  |||  ||||||   |  ||      |||||    |  ||||||
Db     484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
           |    | |||     |||||||||    |  || |||||||  | |||    |  ||
Db     544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603

Qy     451 tacgg 455
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Db     604 TACGG 608
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RESULT   9
US-09-080-285-20
; Sequence 20, Application US/09080285
; Patent No. 6040181
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, John
;    TITLE OF INVENTION:  Regulation of bcl-2 Gene Expression
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Hwy., Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,485
;      FILING DATE:  05-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/124,256
;      FILING DATE:  20-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/840,716
;      FILING DATE:  21-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/288,692
;      FILING DATE:  22-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fortney, Andrew D.
;      REGISTRATION NUMBER:  34,600
;      REFERENCE/DOCKET NUMBER:  3335-070-55 CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (408) 436-2070
;      TELEFAX:  (408) 436-2075
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..717
US-09-080-285-20
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  Query Match             21.5%;  Score 125;  DB 5;  Length 717;
  Best Local Similarity   58.9%;  Pred. No. 1.8e-26;
  Matches  215;  Conservative    0;  Mismatches  150;  Indels    0;  Gaps    0;

Qy      91 gctgggcctggggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctgga 150
           || ||||||| |    |||| |   |       | | ||||  ||| | ||    || ||
Db     244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303

Qy     151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
           ||||| ||      ||| | |||| ||  |||| | ||  || ||   ||||| ||| ||
Db     304 GACGACTTCTCCCGCCGCTACCGCGGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTG 363

Qy     211 accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
           || ||   | | || | |  ||||||  ||  |||    || || || |||   |  ||
Db     364 ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 423

Qy     271 cctaactggggccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagt 330
           ||||||||  |  ||||||| |||||||  || || |  | | ||||||  |||||
Db     424 GTGAACTGGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTCATGTGTGTGGAGAGC 483

Qy     331 gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
           ||||||   || |||  |||  ||||||   |  ||      |||||    |  ||||||
Db     484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543

Qy     391 gagacacgtctggctgactggatccacagcagtggcggctgggcggacttcacagctcta 450
           |    | |||     |||||||||    |  || |||||||  | |||    |  ||
Db     544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603

Qy     451 tacgg 455
           |||||
Db     604 TACGG 608
```

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RESULT  10
5459251-1
;Patent No. 5459251
;    APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.
;    TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
;SEQUENCES
;    NUMBER OF SEQUENCES: 4
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Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          ||||| |  | ||||| ||| | ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  |||||| || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || ||||| |  || || ||  |||| || ||| ||   |||||| | |   ||
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | ||||||  |   | ||||||  |    |  || |     ||||||||    |  ||||
Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||   ||    |  ||    ||        |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
           |||  ||  |      ||  |    || |   |||| | |||||
Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
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RESULT 7
PCT-US94-07089-6
; Sequence 6, Application PC/TUS9407089
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07089
; FILING DATE: CONCURRENTLY FILED
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/081.448
; FILING DATE: 22 JUNE 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..836
PCT-US94-07089-6

Query Match 23.2%; Score 134.6; DB 6; Length 926;
Best Local Similarity 58.3%; Pred. No. 4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

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Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | |||||  || |||  || || ||||||||||    || | ||| ||  | |||  ||
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          ||||| |  | ||||| ||| | ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  |||||| || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || ||||| |  || || ||  |||| || ||| ||   |||||| | |   ||
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | ||||||  |   | ||||||  |    |  || |     ||||||||    |  ||||
Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||   ||    |  ||    ||        |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
           |||  ||  |      ||  |    || |   |||| | |||||
Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
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RESULT 8
US-08-465-485A-20
; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

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Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||| |||||||||||| |||||||||||||||||||||||||||||||||| || |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
          |||||||||||||||||||||||||||||||||||||||
Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579


RESULT   5
US-08-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Craig B.
;    APPLICANT:  Boise, Lawrence H.
;    TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
;    TITLE OF INVENTION:  Compositions and Methods
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  321 No. 5646008th Clark Street, Suite 800
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/081,448
;      FILING DATE:  19930622
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5646008thrup, Thomas E.
;      REGISTRATION NUMBER:  33,268
;      REFERENCE/DOCKET NUMBER:  ARCD090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-744-0090
;      TELEFAX:  312-755-4489
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-081-448-5


  Query Match             23.2%;  Score 134.6;  DB 1;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 4e-29;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
          | ||||| || ||| || || ||||||||||    || | ||| ||  | |||  ||
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
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Qy    248 ccgacgaacttttccaaggggccctaactggggccgtcttgtggcattctttgtctttg 307
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Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
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Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
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Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
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US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Craig B. B.
;    APPLICANT:  Boise, Lawrence H.
;    TITLE OF INVENTION:  VERTEBRATE APOPTOSIS GENE:
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,670A
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/081,448
;      FILING DATE:  22-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Highlander, Steven L.
;      REGISTRATION NUMBER:  37,642
;      REFERENCE/DOCKET NUMBER:  ARCD:090--1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  926 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  135..836
US-08-470-670A-6


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  Best Local Similarity   58.3%;  Pred. No. 4e-29;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-798-897-2


  Query Match             85.6%;  Score 497.4;  DB 2;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 3e-131;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

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RESULT   4
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; Sequence 2, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-2


  Query Match             85.6%;  Score 497.4;  DB 3;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 3e-131;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

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Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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; Sequence 1, Application US/08978523
; Patent No. 5883229
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,523
;      FILING DATE:  herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
```

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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-978-523-1


  Query Match             93.0%;  Score 540.6;  DB 3;  Length 579;
  Best Local Similarity   95.9%;  Pred. No. 2.1e-143;
  Matches  555;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

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RESULT   3
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; Sequence 2, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Searched: 230463 seqs, 64992525 residues

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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	497.4	85.6	579	2	US-08-798-897-2	Sequence 2, Appli
4	497.4	85.6	579	3	US-08-978-523-2	Sequence 2, Appli
5	134.6	23.2	926	1	US-08-081-448-5	Sequence 5, Appli
6	134.6	23.2	926	3	US-08-470-670A-6	Sequence 6, Appli
7	134.6	23.2	926	6	PCT-US94-07089-6	Sequence 6, Appli
8	125	21.5	717	3	US-08-465-485A-20	Sequence 20, Appl
9	125	21.5	717	5	US-09-080-285-20	Sequence 20, Appl
10	125	21.5	4825	7	5459251-1	Patent No. 5459251
11	125	21.5	5086	3	US-08-465-485A-19	Sequence 19, Appl
12	125	21.5	5086	3	US-08-365-486A-14	Sequence 14, Appl
13	125	21.5	5086	5	US-09-080-285-19	Sequence 19, Appl
14	125	21.5	5086	6	PCT-US93-05651-4	Sequence 4, Appli
15	125	21.5	5086	6	PCT-US93-06251-2	Sequence 2, Appli
16	125	21.5	5104	7	5506344-1	Patent No. 5506344
17	123.4	21.2	760	2	US-08-405-702A-11	Sequence 11, Appl
18	123.4	21.2	1846	3	US-08-365-486A-16	Sequence 16, Appl
19	120.2	20.7	1274	3	US-08-470-670A-1	Sequence 1, Appli
20	120.2	20.7	1274	6	PCT-US94-07089-1	Sequence 1, Appli
21	120.2	20.7	1303	1	US-08-081-448-1	Sequence 1, Appli
22	119	20.5	615	3	US-08-465-485A-22	Sequence 22, Appl
23	119	20.5	615	5	US-09-080-285-22	Sequence 22, Appl
24	119	20.5	911	6	PCT-US93-06251-3	Sequence 3, Appli
25	115.8	19.9	831	7	5459251-3	Patent No. 5459251
26	115.8	19.9	831	7	5506344-4	Patent No. 5506344
27	74.8	12.9	623	7	5506344-3	Patent No. 5506344
28	57	9.8	737	1	US-08-081-448-7	Sequence 7, Appli
29	57	9.8	737	3	US-08-470-670A-8	Sequence 8, Appli
30	57	9.8	737	6	PCT-US94-07089-8	Sequence 8, Appli
31	44.4	7.6	5408	2	US-08-471-058-20	Sequence 20, Appl
32	44.4	7.6	5408	5	US-08-471-057-20	Sequence 20, Appl
33	40.6	7.0	624	2	US-08-112-208C-1	Sequence 1, Appli
34	40.6	7.0	624	2	US-08-248-819A-1	Sequence 1, Appli
35	40.6	7.0	624	3	US-08-337-646A-1	Sequence 1, Appli
36	40.6	7.0	624	4	US-08-856-531-1	Sequence 1, Appli
37	40.6	7.0	624	4	US-08-856-034-1	Sequence 1, Appli
38	39.4	6.8	822	2	US-08-616-732A-8	Sequence 8, Appli
39	37.6	6.5	1287	2	US-08-471-058-8	Sequence 8, Appli
40	37.6	6.5	1287	4	US-08-944-530-3	Sequence 3, Appli
41	37.6	6.5	1287	5	US-08-471-057-8	Sequence 8, Appli
42	36.4	6.3	1968	1	US-08-321-071A-17	Sequence 17, Appl
43	36.4	6.3	2094	2	US-08-471-058-6	Sequence 6, Appli
44	36.4	6.3	2094	4	US-08-944-530-1	Sequence 1, Appli
45	36.4	6.3	2094	5	US-08-471-057-6	Sequence 6, Appli

ALIGNMENTS

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RESULT   1
US-08-798-897-1
; Sequence 1, Application US/08798897
; Patent No. 5789201
;  GENERAL INFORMATION:
;    APPLICANT:  Guastella, John
;    TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
;    TITLE OF INVENTION:  Homologue
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 New York Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/798,897
;      FILING DATE:  February 11, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Esmond, Robert W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1483.0140001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  579 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-798-897-1


  Query Match             93.0%;  Score 540.6;  DB 2;  Length 579;
  Best Local Similarity   95.9%;  Pred. No. 2.1e-143;
  Matches  555;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
           ||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Db    425 GTCGCATTGTGGCCTTTTTCTCCTTCGGTGGGGCACTGTGCGTGGAGAGCGTAGACAAGG 484

Qy    341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
          | ||| ||   |||||| | |   ||     |||||| |   | |||||| |    |  |
Db    485 AGATGCAGGTATTGGTGAGTCGGATCGCAACTTGGATGGCCACTTACCTGAATGACCACC 544

Qy    401 tggctgactggatccacagcagtggcggctgggcggacttcacagctctatacggggacg 460
          | |     ||||||||     |  ||||||||||     ||     |  || |||||  ||
Db    545 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGAACTTTACGGAAACA 604

Qy    461 gggccctggaggacgcacggcgtctgcgggagggcaactgggcatgagtgagcacagtgg 520
            ||   |  ||   |||    | |||| ||  |    |||  |    || |
Db    605 ATGCAGCAGCTGAGAGCCGGAAGGGCCAGGAGCGCTTCAACCGATGGTTCCTGACGGGCA 664

Qy    521 tgacgggggccgtgg 535
          ||||    || | ||
Db    665 TGACTCTAGCTGGGG 679


RESULT  15
SSJ001203
LOCUS       SSJ001203     752 bp    mRNA            MAM       10-FEB-1999
DEFINITION  Sus scrofa mRNA for anti-apoptotic Bcl-xL.
ACCESSION   AJ001203
VERSION     AJ001203.1  GI:3288631
KEYWORDS    apoptosis.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Bartling,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1998) Bartling B., Institute of Pathophysiology,
            Martin Luther University, Magdeburger Strasse 18, 06097 Halle,
            GERMANY
REFERENCE   2  (bases 1 to 752)
  AUTHORS   Bartling,B., Hoffmann,J., Holtz,J., Schulz,R., Heusch,G. and
            Darmer,D.
  TITLE     Expression of apoptosis-associated genes in hibernating and stunned
            myocardium of pig
  JOURNAL   Unpublished
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
     CDS             44. .745
                     /note="transmembrane domain: 680-736; Bcl-2 homolgy
                     domains: BH4: 56-115, BH3: 298-343, BH1: 428-487, BH2:
                     581-628"
                     /codon_start=1
                     /protein_id="CAA04597.1"
                     /db_xref="GI:3288632"
                     /db_xref="SPTREMBL:O77737"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
                     AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
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                     VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
                     TLAGVVLLGSLFSRK"
BASE COUNT      178 a    183 c    237 g    154 t
ORIGIN


  Query Match             23.1%;  Score 134.2;  DB 3;  Length 752;
  Best Local Similarity   56.8%;  Pred. No. 1.6e-21;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy    101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
          |||| |      ||   |   |  || | |||||  || |||  || || || |||||||
Db    276 GGGAGGTGATCCCCATGGCTGCAGTGAAGCAAGCGCTGAGGGAGGCGGGCGATGAGTTTG 335

Qy    161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
          |     | | |||  |  | |||  ||||||| |  | |||||  ||| | ||||||||

Db    336 AACTGAGGTACCGGAGGGCATTCAGTGACCTGACGTCCCAGCTCCACATCACCCCAGGGA 395

Qy    221 cagcccagcaacgcttcacccaggtttccgacgaacttttccaaggggggccctaactggg 280
          ||||  | ||  ||||    |||||  |   ||||||| ||||  |  ||    |||||||
Db    396 CAGCGTATCAGAGCTTTGAGCAGGTATTGAACGAACTCTTCCGGGATGGGGTGAACTGGG 455

Qy    281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
          | ||  ||||||| || ||   ||| || |  || ||||| |  |||||  ||  |||| |
Db    456 GTCGCATTGTGGCCTTTTTCTCCTTCGGTGGGGCACTGTGCGTGGAGAGCGTAGACAAGG 515

Qy    341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
          | ||| ||   ||||||| | |   ||     |||||| |   | |||||| |    |  |
Db    516 AGATGCAGGTATTGGTGAGTCGGATCGCAACTTGGATGGCCACTTACCTGAATGACCACC 575

Qy    401 tggctgactggatccacagcagtggcggctgggcggacttcacagctctatacggggacg 460
          | |     ||||||||     |  ||||||||||     ||     |  || |||||  ||
Db    576 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGAACTCTACGGAAACA 635

Qy    461 gggccctggaggacgcacggcgtctgcgggagggcaactgggcatgagtgagcacagtgg 520
            ||   |  ||   |||    | |||  ||  |    |||  |    || |
Db    636 ATGCAGCAGCTGAGAGCCGGAAGGGCCAGGAACGCTTCAACCGATGGTTCCTGACGGGCA 695

Qy    521 tgacgggggccgtgg 535
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Db    696 TGACTCTAGCTGGGG 710


Search completed: July  4, 2000, 01:22:44
Job time: 16645 sec
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Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT 13
HSBCLXL
LOCUS       HSBCLXL       926 bp    mRNA            PRI       26-JUL-1994
DEFINITION  H.sapiens bcl-xL mRNA.
ACCESSION   Z23115 L20121
VERSION     Z23115.1  GI:510900
KEYWORDS    bcl-xL gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   Thompson,C.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
            Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
            60637, USA
REFERENCE   2  (bases 1 to 926)
  AUTHORS   Boise,L.H., Gonzalez-Garcia,M., Postema,C.E., Ding,L., Lindsten,T.,
            Turka,L.A., Mao,X., Nunez,G. and Thompson,C.B.
  TITLE     bcl-x, a bcl-2-related gene that functions as a dominant regulator
            of apoptotic cell death
  JOURNAL   Cell 74 (4), 597-608 (1993)
  MEDLINE   93364977
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="bcl-xL"
                     /dev_stage="Adult"
                     /cell_type="brain"
     gene            135. .836
                     /gene="bcl-xL"
     CDS             135. .836
                     /gene="bcl-xL"
                     /codon_start=1
                     /protein_id="CAA80661.1"
                     /db_xref="GI:510901"
                     /db_xref="SWISS-PROT:Q07817"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESE
                     METPSAINGNPSWHLADSPAVNGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
                     TVAGVVLLGSLFSRK"
BASE COUNT      220 a    249 c    264 g    193 t
ORIGIN


  Query Match           23.2%;  Score 134.6;  DB 9;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 1.2e-21;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattctttgtctttg 307
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT 14
AF216205
LOCUS       AF216205      720 bp    mRNA            MAM       11-FEB-2000
DEFINITION  Sus scrofa anti-apoptotic regulator Bcl-xL (bcl-xL) mRNA, complete
            cds.
ACCESSION   AF216205
VERSION     AF216205.1  GI:6959766
KEYWORDS    .
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Lee,T.L. and Canty,J.M.
  TITLE     PCR Cloning of a Porcine bcl-xL cDNA from Heart
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Lee,T.L. and Canty,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main
            Street, Buffalo, NY 14214-3000, USA
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /tissue_type="heart"
     gene            1. .720
                     /gene="bcl-xL"
     CDS             13. .714
                     /gene="bcl-xL"
                     /codon_start=1
                     /product="anti-apoptotic regulator Bcl-xL"
                     /protein_id="AAF33212.1"
                     /db_xref="GI:6959767"
                     /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
                     AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
                     RAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
                     VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
                     TLAGVVLLGSLFSRK"
BASE COUNT      170 a    176 c    229 g    145 t
ORIGIN


  Query Match           23.1%;  Score 134.2;  DB 3;  Length 720;
  Best Local Similarity   56.8%;  Pred. No. 1.6e-21;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy    101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
Db    245 GGGAGGTGATCCCCATGGCTGCAGTGAAGCAAGCGCTGAGGGAGGCGGGCGATGAGTTTG 304

Qy    161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
Db    305 AACTGAGGTACCGGAGGGCATTCAGTGACCTGACGTCCCAGCTCCACATCACCCCAGGGA 364

Qy    221 cagcccagcaacgcttcacccaggtttccgacgaacttttccaaggggggccctaactggg 280
Db    365 CAGCGTATCAGAGCTTTGAGCAGGTAGTGAACGAACTCTTCCGGGATGGGGTGAACTGGG 424

Qy    281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
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                    DLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVG
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                    VLLLGSLLSRK"
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     polyA_signal   1161. .1166
BASE COUNT      249 a    324 c    374 g    237 t
ORIGIN


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  Best Local Similarity   58.3%;  Pred. No. 1.7e-22;
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Db    414 TGAGGCAGGCGCTGAGAGATGCGGGGGATGAGTTTGAGCTGAGGTACCGGAGGGCTTTCA 473

Qy    185 ctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccagg 244
            |||||  || | |||||  ||| | |||||  ||| | ||  | ||  ||||    ||||
Db    474 GCGACCTCACCTCCCAGCTCCACATCACCCCTGGCACGGCGTACCAGAGCTTTGAGCAGG 533

Qy    245 tttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattctttgtct 304
          |     | |||||  |||||  |  ||    |||||||| ||  | |||||  |||||   ||
Db    534 TAGTGAATGAACTCTTCCATGATGGTGTGAACTGGGGGCGCATCGTGGCTTTCTTCTCCT 593

Qy    305 ttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaag 364
          | || |  ||  |||| |  ||||| ||  |||| || |||  |    |||||||||
Db    594 TCGGAGGGGCTTTGTGCGTGGAGAGCGTGGACAAGGAGATGCGGGTACTGGTGGGACGCA 653

Qy    365 tccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtg 424
          |   |  ||||||     | ||| ||       | ||| | |  |||||||||    | ||
Db    654 TTGTGTCTTGGATGACCACGTACTTGACCGACCATCTAGATCCCTGGATCCAGGAGAATG 713

Qy    425 gcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtc 484
          |||||||||  |  |||    | ||| || ||| ||    ||     |  ||     ||
Db    714 GCGGCTGGGAGCGCTTTGTGGATCTGTATGGGAACAACGCTGCTGCCGAGCTGAGGAAGG 773

Qy    485 tgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcact 539
            | ||||  |  |     |||  |   ||| | || ||| | |||||  |  ||
Db    774 GCCAGGAGACCTTCAACAAATGGCTCCTCACCGGGGCGACCGTGGCCGGAGTGCT 828


RESULT  11
AR054021
LOCUS       AR054021      926 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 6 from patent US 5834309.
ACCESSION   AR054021
VERSION     AR054021.1  GI:5978883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   Thompson,C.B., Boise,L.H. and Nunez,G.
  TITLE     Vertebrate apoptosis gene: compositions and methods
  JOURNAL   Patent: US 5834309-A 6 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .926
                     /organism="unknown"
BASE COUNT      220 a    249 c    264 g    193 t
ORIGIN


  Query Match             23.2%;  Score 134.6;  DB 5;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 1.2e-21;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
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Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          ||||| |  | ||||| ||| | ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  ||||||| || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
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Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||  ||    |  ||   ||       |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
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Db    754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798


RESULT  12
I52011
LOCUS       I52011        926 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 5 from patent US 5646008.
ACCESSION   I52011
VERSION     I52011.1  GI:2473212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   Thompson,C.B., Boise,L.H. and Nunez,G.
  TITLE     Vertebrate apoptosis gene: compositions and methods
  JOURNAL   Patent: US 5646008-A 5 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .926
                     /organism="unknown"
BASE COUNT      220 a    249 c    264 g    193 t
ORIGIN


  Query Match             23.2%;  Score 134.6;  DB 5;  Length 926;
  Best Local Similarity   58.3%;  Pred. No. 1.2e-21;
  Matches  236;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
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Db    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453

Qy    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
          ||||| |  | ||||| ||| | ||||||||  ||||  | ||  ||||    |||||
Db    454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513

Qy    248 ccgacgaacttttccaaggggccctaactggggccgtcttgtggcattctttgtctttg 307
            | ||||| ||||  |  ||    |||||||| ||  ||||||| || ||   ||| |
Db    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573

Qy    308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
          | |  || ||||| |  || || ||  |||| || ||| ||   |||||| | |   ||
Db    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633

Qy    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
            | |||||| |   | |||||| |    |  || |     ||||||||    | ||||
Db    634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693

Qy    428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
          ||||||     ||    |  || || ||| ||  ||    |  ||   ||       |
Db    694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753

Qy    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
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Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db  90001 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 90060

Qy    241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
          ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db  90061 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 90120

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
          |||||||||||||| |||||||||||||||||||||||| || ||||| ||  ||||||||
Db  90121 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 90180

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||| |  ||||||||||||||||||||
Db  90181 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCAGCTGGCTGACTGGATCCACAGC 90240

Qy    421 agtggcggctggg 433
          ||||| |||||||
Db  90241 AGTGGGGGCTGGG 90253
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RESULT  9
XLR1
LOCUS       XLR1          749 bp    mRNA            VRT       01-JUL-1997
DEFINITION  X.laevis R1 mRNA.
ACCESSION   X82462
VERSION     X82462.1  GI:575421
KEYWORDS    xR1 gene.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
            Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   Cruz-Reyes,J. and Tata,J.R.
  TITLE     Cloning, characterization and expression of two Xenopus bcl-2-like
            cell-survival genes
  JOURNAL   Gene 158 (2), 171-179 (1995)
  MEDLINE   95331613
REFERENCE   2  (bases 1 to 749)
  AUTHORS   Cruz-Reyes,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
            Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
            1AA, UK
FEATURES             Location/Qualifiers
     source          1. .749
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /dev_stage="28-30 (tailbud tadpole)"
                     /clone_lib="lambda ZapII:R1"
                     /clone="pKS+:xR1"
     gene            3. .689
                     /gene="xR1"
     CDS             3. .689
                     /gene="xR1"
                     /note="Protein sequence is in conflict with the conceptual
                     translation"
                     /codon_start=1
                     /protein_id="CAA57845.1"
                     /db_xref="GI:1334682"
                     /db_xref="SWISS-PROT:Q91827"
                     /translation="LNPKKKENNGVKNGDREKQHETGNTIFRGSPDKYLTEQGWMAQS
                     DLGSRALVEDLVRYKLCQRSLVPEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQ
                     IHVTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDW
                     MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL
                     MTVGALFASK"
BASE COUNT      203 a    146 c    224 g    176 t
ORIGIN
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  Query Match             40.2%;  Score 233.8;  DB 4;  Length 749;
  Best Local Similarity   68.1%;  Pred. No. 1.2e-44;
  Matches  325;  Conservative    0;  Mismatches  152;  Indels    0;  Gaps    0;

Qy    105 aggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttgagac 164
          |||  |||| ||    |  ||||    || ||||| ||||| || || || ||||||
Db    212 AGGAGCAGCATCCTGTGCTTTGCATTCGGCTATGCGTGCTGCAGGGGATGAATTTGAGGA 271

Qy    165 ccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggctcagc 224
          || ||| | |   | |||  |||  |  || | ||| | || |||||||| ||| ||||
Db    272 GCGATTCAGACAAGCATTCAGTGAGATCTCCACACAGATCCATGTGACCCCCGGCACAGC 331

Qy    225 ccagcaacgcttcacccaggtttccgacgaacttttccaaggggccctaactggggccg 284
          |   ||||||  |  | ||  | |     || |||||||| ||    || ||||| ||
Db    332 ATATGCACGCTTTGCAGAAGTAGCAGGTAGCCTATTCCAAGGTGGGGTGAATTGGGGTCG 391

Qy    285 tcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaagaaat 344
          | || ||||| ||||| ||||| || || ||||||||||||||||||||||| || ||
Db    392 CATAGTTGCATTTTTTGTTTTTGGTGCCGCGCTGTGTGCTGAGAGTGTCAACAAGGAGAT 451

Qy    345 ggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtctggc 404
          |   ||| |  ||  ||   |||| || ||||| ||| | || ||||||||   |||
Db    452 GTCCCCTCTTCTGCCACGGATCCAAGACTGGATGGTGACATATCTGGAGACAAACCTGAG 511

Qy    405 tgactggatccacagcagtggcggctgggcggacttcacagctctatacggggacggggc 464
          |||||||| || |||| ||| ||||||   |  ||   | ||||||| ||||| || ||
Db    512 AGACTGGATTCAGAGCAATGGTGGCTGGAATGGGTTTCTAACTCTATATGGGGATGGTGC 571

Qy    465 cctggaggacgcacggcgtctgcgggagggcaactgggcatgagtgagcacagtggtgac 524
          | | || || ||  || | |  || ||||| || ||||||| | |||  || ||  | ||
Db    572 CATAGAAGAAGCCAGGAGGCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAAC 631

Qy    525 gggggccgtggcactgggggccctggtaactgtaggggccttttttgctagcaagtg 581
          || || ||||| ||||| ||  || | || |||||||||||| ||||| ||||||||
Db    632 TGGAGCTGTGGCTCTGGGTGCTTTGATGACAGTAGGGGCCTTGTTTGCCAGCAAGTG 688
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RESULT  10
GGU26645
LOCUS       GGU26645     1184 bp    mRNA            VRT       06-SEP-1996
DEFINITION  Gallus gallus bcl-x mRNA, complete cds.
ACCESSION   U26645
VERSION     U26645.1  GI:1522678
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
            Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1184)
  AUTHORS   Vilagrasa,X., Mezquita,J. and Mezquita,C.
  TITLE     Gallus domesticus bcl-x mRNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1184)
  AUTHORS   Vilagrasa,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-1995) Xavier Vilagrasa, Faculty of Medicine.
            University of Barcelona, Molecular Genetics Research Group,
            Casanova 143, Barcelona 08036, Spain
COMMENT     On Sep 6, 1996 this sequence version replaced gi:1381039.
FEATURES             Location/Qualifiers
     source          1. .1184
                     /organism="Gallus gallus"
                     /strain="Hubbard White Mountain"
                     /db_xref="taxon:9031"
                     /sex="male"
                     /tissue_type="testis"
     gene            170. .859
                     /gene="bcl-x"
     CDS             170. .859
                     /gene="bcl-x"
                     /codon_start=1
                     /protein_id="AAB07677.1"
                     /db_xref="GI:1522679"
                     /translation="MSSSNRELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMD
                     SVLNGSPSWHPPAGHVVNGATVHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFS
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Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          || ||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| |||||| |||||||| || ||||||||||||||||||||| ||||||||||||
Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
          ||||| |||||| |||||||| |||||||||||| |||||||||||| ||||| || ||||||
Db    241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
          |||||||||||||| ||||||||||||||||||||||| || ||||| ||  ||||||||
Db    301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
          ||||| ||||| ||||| |||||||||||||||| || ||||||||||||||||||||||
Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
          ||||| |||||||||||| ||||||||||||||||||||||||||||||||||| || |||
Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
          |||||||||||||| |||||||||| |||||| |||||| ||||||||||||||||||||
Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT   8
CNS0000B
LOCUS       CNS0000B   196287 bp    DNA             PRI       27-OCT-1999
DEFINITION  Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
            RPCI-11 library from chromosome 14 of Homo sapiens (Human),
            complete sequence.
ACCESSION   AL049829
VERSION     AL049829.3  GI:6138746
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 196287)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     On Oct 28, 1999 this sequence version replaced gi:4972127.
            IMPORTANT: This sequence is unfinished and does not necessarly
            represent the correct sequence. Work on the sequence is in progress
            and the release of this data is based on the understanding that the
            sequence may change as work continue. The sequence may be
            contaminated with foreign sequence from E.coli, yeast, vector,
            phage, etc.XX.
FEATURES             Location/Qualifiers
     source          1. .196287
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone_lib="RPCI-11"
                     /clone="R-124D2"
     STS             78257. .78396
                     /standard_name="AA908790"
                     /note="matching EMBL:AA908790; Identified using the e-PCR
                     software (G. Schuler)"
     STS             80431. .80564
                     /standard_name="AA167748"
                     /note="matching EMBL:AA167748; Identified using the e-PCR
                     software (G. Schuler)"
     STS             82162. .82297
                     /standard_name="H79035"
                     /note="matching EMBL:H79035; Identified using the e-PCR
                     software (G. Schuler)"
     STS             93575. .93803
                     /standard_name="AA007328"
                     /note="matching EMBL:AA007328; Identified using the e-PCR
                     software (G. Schuler)"
     STS             107753. .107946
                     /standard_name="R94929"
                     /note="matching EMBL:R94929; Identified using the e-PCR
                     software (G. Schuler)"
     STS             107991. .108176
                     /standard_name="D11677"
                     /note="matching EMBL:D11677; Identified using the e-PCR
                     software (G. Schuler)"
     STS             128383. .128521
                     /standard_name="H22648"
                     /note="matching EMBL:H22648; Identified using the e-PCR
                     software (G. Schuler)"
     STS             128415. .128539
                     /standard_name="R87257"
                     /note="matching EMBL:R87257; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138457. .138733
                     /standard_name="R59134"
                     /note="matching EMBL:R59134; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138504. .138653
                     /standard_name="M78864"
                     /note="matching EMBL:M78864; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138563. .138642
                     /standard_name="M78986"
                     /note="matching EMBL:M78986; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138563. .138672
                     /standard_name="M78946"
                     /note="matching EMBL:M78946; Identified using the e-PCR
                     software (G. Schuler)"
     STS             138800. .138921
                     /standard_name="H72023"
                     /note="matching EMBL:H72023; Identified using the e-PCR
                     software (G. Schuler)"
     STS             161612. .161756
                     /standard_name="AA452257"
                     /note="matching EMBL:AA452257; Identified using the e-PCR
                     software (G. Schuler)"
     STS             194799. .194898
                     /standard_name="N91549"
                     /note="matching EMBL:N91549; Identified using the e-PCR
                     software (G. Schuler)"
BASE COUNT    50873 a  45668 c  47123 g  52623 t
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  Best Local Similarity   90.1%;  Pred. No. 2.9e-75;
  Matches  390;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy      1 atgccgacccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| ||||||||||||  ||||||||||||| ||||| ||||| ||||||||||| |||
Db  89821 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 89880

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | ||||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db  89881 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 89940

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          |||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db  89941 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 90000
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Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   6
D87461
LOCUS       D87461       3542 bp    mRNA            PRI       10-JUL-1997
DEFINITION  Human mRNA for KIAA0271 gene, complete cds.
ACCESSION   D87461
VERSION     D87461.1  GI:1944417
KEYWORDS    KIAA0271.
SOURCE      Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA,
            clone_lib:pSPORT 1 clone:HA6752.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3542)
  AUTHORS   Nomura,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo
            Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3
            Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
REFERENCE   2  (sites)
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes.VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from human cell line KG-1 and brain
  JOURNAL   Unpublished (1996)
REFERENCE   3  (sites)
  AUTHORS   Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
            Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
  TITLE     Prediction of the coding sequences of unidentified human genes. VI.
            The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
            analysis of cDNA clones from cell line KG-1 and brain
  JOURNAL   DNA Res. 3 (5), 321-329 (1996)
  MEDLINE   97191544
FEATURES             Location/Qualifiers
     source          1. .3542
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="KG-1"
                     /cell_type="myloblast"
                     /clone="HA6752"
                     /clone_lib="pSPORT 1"
                     /sex="male"
                     /tissue_type="brain"
     gene            177. .758
                     /gene="KIAA0271"
     CDS             177. .758
                     /gene="KIAA0271"
                     /note="similar to human transforming protein bcl-2
                     (A24428)"
                     /codon_start=1
                     /protein_id="BAA19666.1"
                     /db_xref="GI:1944418"
                     /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
                     GAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
BASE COUNT      804 a    817 c   1030 g    891 t
ORIGIN


  Query Match           86.5%;  Score 502.6;  DB 9;  Length 3542;
  Best Local Similarity   91.6%;  Pred. No. 3.6e-107;
  Matches  532;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| |||||||||||||  |||||||||||||| ||||| ||||| |||||||||||| |||
Db    177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db    237 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 296

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
          |||||||||||||||||||||||| |||||||| ||||| |||||||| ||||| ||||||
Db    297 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
          |||||||| ||||| |||||||| || |||||||||||||||||||| ||||||||||||
Db    357 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC 416

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
          ||||| ||||| |||||||| |||||||||| |||||||||| ||||| || ||||||
Db    417 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 476

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    477 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    537 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db    597 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 656

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    657 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 716

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
          |||||||||||||||||||||||||||||||||||||||||
Db    717 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 757


RESULT   7
AR020780
LOCUS       AR020780      579 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 2 from patent US 5789201.
ACCESSION   AR020780
VERSION     AR020780.1  GI:3975395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Guastella,J.
  TITLE     Genes coding for bcl-y a bcl-2 homologue
  JOURNAL   Patent: US 5789201-A 2 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="unknown"
BASE COUNT      106 a    154 c    208 g    111 t
ORIGIN


  Query Match           85.6%;  Score 497.4;  DB 5;  Length 579;
  Best Local Similarity   91.2%;  Pred. No. 7.5e-106;
  Matches  528;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

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Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTTTGTAGGTTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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DEFINITION  Sequence 1 from patent US 5789201.
ACCESSION   AR020779
VERSION     AR020779.1  GI:3975394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Guastella,J.
  TITLE     Genes coding for bcl-y a bcl-2 homologue
  JOURNAL   Patent: US 5789201-A 1 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .579
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BASE COUNT      111 a    157 c    198 g    113 t
ORIGIN
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  Query Match             93.0%;  Score 540.6;  DB 5;  Length 579;
  Best Local Similarity   95.9%;  Pred. No. 7e-116;
  Matches  555;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db     61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db    241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db    421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy    481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy    541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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Db    541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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RESULT   5
HSU59747
LOCUS       HSU59747      582 bp    mRNA            PRI       29-SEP-1996
DEFINITION  Human Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59747
VERSION     U59747.1  GI:1572492
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q11"
     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
                     /gene="bcl-w"
                     /note="promotes cell survival"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAB09055.1"
                     /db_xref="GI:1572493"
                     /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
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BASE COUNT      104 a    156 c    211 g    111 t
ORIGIN
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  Query Match             87.1%;  Score 505.8;  DB 10;  Length 582;
  Best Local Similarity   91.9%;  Pred. No. 8.4e-108;
  Matches  534;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy      1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
          ||| ||||||||||||  ||||||||||||| ||||| ||||| |||||||||||| |||
Db      1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

Qy     61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
          | |||||||||||||||||||||||||||||||| || ||||| |||||||| || |||
Db     61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120

Qy    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db    121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180

Qy    181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db    181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy    241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db    241 CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300

Qy    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db    301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

Qy    361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db    361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420

Qy    421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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                     /note="mRNA destabilization element"
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ORIGIN


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  Best Local Similarity   97.8%;  Pred. No. 1.5e-120;
  Matches  568;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

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Db     179 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 238

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db     239 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 298

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Db     299 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 358

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db     359 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 418

Qy     241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
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Db     419 CAGGTTTCCGACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 478

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 538

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db     539 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 598

Qy     421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db     599 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 658

Qy     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db     659 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 718

Qy     541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db     719 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 759


RESULT   3
AF096291
LOCUS       AF096291      582 bp    mRNA            ROD       15-OCT-1998
DEFINITION  Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   AF096291
VERSION     AF096291.1  GI:3747129
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Differential expression of Bcl-w and Bcl-x mRNA in the developing
            and adult nervous system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Hamner,S., Skoglosa,Y. and Lindholm,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
            University, Box 587, BMC, Uppsala 751 23, Sweden
FEATURES             Location/Qualifiers
     source          1. .582
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                     /tissue_type="brain"
                     /dev_stage="postnatal"
     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
                     /gene="bcl-w"
                     /note="Bcl-2 family member"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAC64200.1"
                     /db_xref="GI:3747130"
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BASE COUNT      111 a    157 c    200 g    114 t
ORIGIN


  Query Match             93.7%;  Score 544.2;  DB 12;  Length 582;
  Best Local Similarity   96.0%;  Pred. No. 1e-116;
  Matches  558;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

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Db       1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
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Db      61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
           |||||||||||||||||||||| |||||||||||||||||||||| ||||| ||||||
Db     121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttt 300
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Db     241 CAGGTTTCCGACGAACTTTTCCAAGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Db     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
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Db     361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420

Qy     421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db     421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db     481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540

Qy     541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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Db     541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTG 581


RESULT   4
AR020779
LOCUS       AR020779      579 bp    DNA             PAT       05-DEC-1998
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RESULT   1
MMU59746
LOCUS       MMU59746      582 bp    mRNA            ROD       29-SEP-1996
DEFINITION  Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION   U59746
VERSION     U59746.1  GI:1572494
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,
            Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.
  TITLE     bcl-w, a novel member of the bcl-2 family, promotes cell survival
  JOURNAL   Oncogene 13 (4), 665-675 (1996)
  MEDLINE   96358615
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
            Cory,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
            Eliza Hall Institute of Medical Research, PO Royal Melbourne
            Hospital, Parkville, Victoria 3050, Australia
FEATURES             Location/Qualifiers
     source          1. .582
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     gene            1. .582
                     /gene="bcl-w"
     CDS             1. .582
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                     /note="promotes cell survival; Bcl-2 homolog"
                     /codon_start=1
                     /product="Bcl-w"
                     /protein_id="AAB09056.1"
                     /db_xref="GI:1572495"
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                     AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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BASE COUNT      107 a    158 c    200 g    117 t
ORIGIN
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  Query Match             96.4%;  Score 560.2;  DB 12;  Length 582;
  Best Local Similarity   97.8%;  Pred. No. 2e-120;
  Matches  568;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
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Qy      61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
           | |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120

Qy     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180

Qy     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Db     181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

Qy     241 caggtttccgacgaacttttccaaggggggccctaactggggccgtcttgtggcattcttt 300
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Db     241 CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300

Qy     301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360

Qy     361 caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
           ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420

Qy     421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Db     421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480

Qy     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
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Db     481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540

Qy     541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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RESULT   2
AF030769
LOCUS       AF030769     3476 bp    mRNA            ROD       16-NOV-1997
DEFINITION  Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
ACCESSION   AF030769
VERSION     AF030769.1  GI:2623249
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3476)
  AUTHORS   Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
            MacGregor,G.R.
  TITLE     Bcl-w is required for testis homeostasis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3476)
  AUTHORS   Ross,A.J. and MacGregor,G.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
            University, 1462 Clifton Road, Atlanta, GA 30322, USA
FEATURES             Location/Qualifiers
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                     /number=4
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2000, 01:21:54 ; Search time 888.39 Seconds
(without alignments)
-636.198 Million cell updates/sec

Title: US-09-155-327B-8
Perfect score: 581
Sequence: 1 atgccgaccccagcctcaac.....gccttttttgctagcaagtg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
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14: gb_sy:*
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56: gb_htg12:*
57: gb_htg13:*
58: gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.2	96.4	582	12	MMU59746	U59746 Mus musculu
2	560.2	96.4	3476	12	AF030769	AF030769 Mus muscu
3	544.2	93.7	582	12	AF096291	AF096291 Rattus no
4	540.6	93.0	579	5	AR020779	AR020779 Sequence
5	505.8	87.1	582	10	HSU59747	U59747 Human Bcl-w
6	502.6	86.5	3542	9	D87461	D87461 Human mRNA
7	497.4	85.6	579	5	AR020780	AR020780 Sequence
8	364.2	62.7	196287	10	CNS0000B	AL049829 Human chr
9	233.8	40.2	749	4	XLR1	X82462 X.laevis R1
10	138.2	23.8	1184	4	GGU26645	U26645 Gallus gall
11	134.6	23.2	926	5	AR054021	AR054021 Sequence
12	134.6	23.2	926	5	I52011	I52011 Sequence 5
13	134.6	23.2	926	9	HSBCLXL	Z23115 H.sapiens b
14	134.2	23.1	720	3	AF216205	AF216205 Sus scrof
15	134.2	23.1	752	3	SSJ001203	AJ001203 Sus scrof
16	131.8	22.7	764	12	RNU10579	U10579 Rattus norv
17	131.8	22.7	1742	12	RNU72350	U72350 Rattus norv
18	131.8	22.7	2232	12	RNCBLXLS	X82537 R.norvegicu
19	127	21.9	708	12	RNU34964	U34964 Rattus norv
20	127	21.9	726	12	RNU34963	U34963 Rattus norv
21	127	21.9	726	12	S76513	S76513 bcl-x=apopt
22	126.8	21.8	723	10	HSU72398	U72398 Human Bcl-x
c 23	126.8	21.8	74673	42	AC016218	AC016218 Homo sapi
24	126.8	21.8	151029	33	HSJ857M17	AL117381 Homo sapi
25	126.6	21.8	687	3	BTU92434	U92434 Bos taurus
26	126.4	21.8	699	12	MMBCLXL	X83574 M.musculus
27	126.4	21.8	702	12	MMU10101	U10101 Mus musculu
28	126.4	21.8	979	12	MUSBCLX	L35049 Mus musculu
29	126.4	21.8	1466	12	MMU51278	U51278 Mus musculu
30	126.4	21.8	5771	14	AF060226	AF060226 Eukaryoti
31	125	21.5	717	5	AR052622	AR052622 Sequence
32	125	21.5	765	5	A76121	A76121 Sequence 1
33	125	21.5	5086	5	AR052621	AR052621 Sequence
34	125	21.5	5086	5	AR054008	AR054008 Sequence
35	125	21.5	5086	9	HUMBCL2A	M13994 Human B-cel
36	125	21.5	5105	5	I08038	I08038 Sequence 1
37	125	21.5	6030	9	HUMBCL2C	M14745 Human bcl-2
38	123.8	21.3	1179	12	RATBCL2A	L14680 Rattus norv
39	123.4	21.2	760	5	AR021160	AR021160 Sequence
40	123.4	21.2	1846	5	AR054009	AR054009 Sequence
41	123.4	21.2	1846	9	HSBCL2IG	X06487 H.sapiens m
42	120.2	20.7	1274	4	GGBCLX	Z23110 G.gallus bc
43	120.2	20.7	1274	5	AR054019	AR054019 Sequence
44	120.2	20.7	1303	5	I52010	I52010 Sequence 1
45	120.2	20.7	1748	12	RNU72349	U72349 Rattus norv

ALIGNMENTS

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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   ---------------------------------------------------------------------------
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DR   HSSP; Q16611; 1BXL.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane.
FT   DOMAIN       74     88       BH3.
FT   DOMAIN      117    136       BH1.
FT   DOMAIN      169    184       BH2.
FT   TRANSMEM    188    205       POTENTIAL.
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  Best Local Similarity  31.5%;  Pred. No. 2.28e-26;
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DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK).
GN   BAK1 OR BAK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-CELL;
RX   MEDLINE; 95231652.
RA   Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,
RA   Grinham C.J., Martinou J.C., Brown R.;
RT   "Cloning of a bcl-2 homologue by interaction with adenovirus E1B
RT   19K.";
RL   Nature 374:731-733(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95231653.
RA   Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,
RA   Evan G.I., Guild B.C.;
RT   "Induction of apoptosis by the Bcl-2 homologue Bak.";
RL   Nature 374:733-736(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95231654.
RA   Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA   Tomei L.D., Barr P.J.;
RT   "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT   Bak.";
RL   Nature 374:736-739(1995).
RN   [4]
RP   SEQUENCE OF 96-206 FROM N.A.
RA   Eguchi H., Hayashi S.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
RX   MEDLINE; 96091131.
RA   Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA   Elangovan B., Chinnadurai G., Lutz R.J.;
RT   "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell
RT   death and protein binding functions.";
RL   EMBO J. 14:5589-5596(1995).
RN   [6]
RP   STRUCTURE BY NMR OF 72-87.
RX   MEDLINE; 97172562.
RA   Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA   Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA   Thompson C.B., Fesik S.W.;
RT   "Structure of Bcl-xL-Bak peptide complex: recognition between
RT   regulators of apoptosis.";
RL   Science 275:983-986(1997).
CC   -!- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC       PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC       REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC   -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC       X(L).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC       HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC   -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
CC       THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
CC       APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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DR   PROSITE; PS01259; BH3; 1.
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DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; 3D-structure.
FT   DOMAIN       74     88       BH3.
FT   DOMAIN      117    136       BH1.
FT   DOMAIN      169    184       BH2.
FT   TRANSMEM    188    205       POTENTIAL.
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AC   Q13014;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   BCL-2 HOMOLOGOUS ANTAGONIST/KILLER 2 (APOPTOSIS REGULATOR BAK-2).
GN   BAK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95231654.
RA   Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA   Tomei L.D., Barr P.J.;
RT   "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT   Bak.";
RL   Nature 374:736-739(1995).
CC   -!- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
CC       PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
CC       REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC   -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC       X(L).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC       HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC   -!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
CC       THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
CC       APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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RL   Nucleic Acids Res. 20:4187-4192(1992).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC   or send an email to license@isb-sib.ch).
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DR   EMBL; M16506; AAA37281.1; -.
DR   PIR; A25960; TVMSA1.
DR   PIR; B25960; TVMSB1.
DR   PIR; E37332; E37332.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:88138; BCL2.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   VARSPLIC    193    236       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                GHK -> VGACLVE (IN ISOFORM BCL-2-BETA).
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Db    136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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Qy     88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147

Db    196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
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Qy    148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT   13
ID   AR11_XENLA     STANDARD;      PRT;   204 AA.
AC   Q91828;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR R11 (XR11).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC   Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEAD;
RX   MEDLINE; 95331613.
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82461; CAA57844.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane.
FT   DOMAIN       101    120       BH1.
FT   DOMAIN       152    167       BH2.
FT   TRANSMEM     181    198       POTENTIAL.
SQ   SEQUENCE   204 AA;  23379 MW;  3BFC6BE6DDA4CA03 CRC64;

  Query Match           39.4%;  Score 546;  DB 1;  Length 204;
  Best Local Similarity  46.7%;  Pred. No. 2.78e-96;
  Matches    71;  Conservative   31;  Mismatches  48;  Indels   2;  Gaps   2;

Db     46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
          | |: :|   : : ||:  | :||| |::|:||||::|||:|  :||| | ||  |||:
Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    106 GTNWGRIVAFFSFGRALCVESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
          | ||||:|||| || ||| || ||||  |: :: :|:| |||  |  |:: :|||  | :
Qy     90 GPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149

Db    166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
          |||  |  ::|  :|   : :: |: ||  ||
Qy    150 LYGDGALEDARRLREG-NWAVSTVV-TGAVAL 179


RESULT   14
ID   BAK_HUMAN      STANDARD;      PRT;   211 AA.
AC   Q16611; Q92533;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
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RX   MEDLINE; 92096610.
RA   Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT   "Frequent incidence of somatic mutations in translocated BCL2
RT   oncogenes of non-Hodgkin's lymphomas.";
RL   Blood 79:229-237(1992).
RN   [6]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE; 91066924.
RA   Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.;
RT   "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT   programmed cell death.";
RL   Nature 348:334-336(1990).
RN   [7]
RP   MUTAGENESIS.
RX   MEDLINE; 94239528.
RA   Yin X.-M., Oltvai Z.N., Korsmeyer J.;
RT   "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT   apoptosis and heterodimerization with Bax.";
RL   Nature 369:321-323(1994).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
CC       II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
CC       T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
CC       REGIONS.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M13994; AAA51813.1; ALT_SEQ.
DR   EMBL; M13995; AAA51814.1; ALT_SEQ.
DR   EMBL; M14745; AAA35591.1; -.
DR   EMBL; X06487; CAA29778.1; -.
DR   EMBL; S72602; AAD14111.1; ALT_SEQ.
DR   PIR; A29409; TVHUA1.
DR   PIR; B29409; TVHUB1.
DR   PIR; A24428; TVHUBC.
DR   PIR; C37332; C37332.
DR   PIR; D37332; D37332.
DR   HSSP; P53563; 1AF3.
DR   MIM; 151430; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
KW   Mitochondrion; Chromosomal translocation; Polymorphism;
KW   Disease mutation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       93    107       BH3.
FT   DOMAIN      136    155       BH1.
FT   DOMAIN      187    202       BH2.
FT   TRANSMEM    212    233       POTENTIAL.
FT   VARSPLIC    196    239       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
FT   MUTAGEN     145    145       G->A: NO HETERODIMERIZATION WITH BAX, AND
FT                                LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     188    188       W->A: NO HETERODIMERIZATION WITH BAX, AND
FT                                LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   VARIANT       7      7       T -> S.
FT                                /FTId=VAR_000827.
FT   VARIANT      59     59       P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                MUTATION).
FT                                /FTId=VAR_000828.
FT   VARIANT      93     93       V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                MUTATION).
FT                                /FTId=VAR_000829.
FT   CONFLICT     48     48       I -> F (IN REF. 4).
FT   CONFLICT     59     59       P -> T (IN REF. 3).
FT   CONFLICT    117    117       S -> R (IN REF. 3).
FT   CONFLICT    129    129       R -> C (IN REF. 4).
SQ   SEQUENCE   239 AA;  26266 MW;  3C49F2B714DC9CCB CRC64;

  Query Match           40.1%;  Score 556;  DB 1;  Length 239;
  Best Local Similarity  43.3%;  Pred. No. 1.27e-98;
  Matches   71;  Conservative   46;  Mismatches  41;  Indels   6;  Gaps   4;

Db     81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
           :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
          | ||||:|||| ||: :| ||||:|| ||| :  |: ||: :|  ||: :|||  |
Qy     90 GPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149

Db    201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
          |||  ::   | | : :| :: |::: |: :|| :|:||::: |
Qy    150 LYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT   12
ID   BCL2_MOUSE     STANDARD;      PRT;   236 AA.
AC   P10417; P10418;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=LIVER;
RX   MEDLINE; 87187643.
RA   Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT   "Molecular analysis of mbcl-2: structure and expression of the murine
RT   gene homologous to the human gene involved in follicular lymphoma.";
RL   Cell 49:455-463(1987).
RN   [2]
RP   REVISIONS TO 221-222.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
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RC   TISSUE=BRAIN;
RX   MEDLINE; 94193015.
RA   Sato T., Irie S., Krajewski S., Reed J.C.;
RT   "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL   Gene 140:291-292(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY;
RX   MEDLINE; 95129487.
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [3]
RP   SEQUENCE OF 19-172 FROM N.A.
RX   MEDLINE; 95059917.
RA   Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA   Lindholm D.;
RT   "bcl-2 messenger RNA is localized in neurons of the developing and
RT   adult rat brain.";
RL   Neuroscience 61:165-177(1994).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA.
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX
CC       REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
CC       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
CC       DIFFER AT THEIR C-TERMINAL ENDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH
CC       HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN,
CC       EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULB,
CC       GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI,
CC       CEREBELLAR GRANULE NEURONS, AND IN EPENDYMAL CELLS. IN PRENATAL
CC       BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM
CC       AND IN THE CORTICAL PLATE.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L14680; AAA53662.1; -.
DR   EMBL; U34964; AAA77687.1; -.
DR   EMBL; S74122; CAB33200.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   CONFLICT     42     42       A -> R (IN REF. 2).
FT   CONFLICT    157    157       E -> G (IN REF. 1).
FT   CONFLICT    164    164       S -> Y (IN REF. 2).
FT   CONFLICT    212    212       L -> Q (IN REF. 2).
SQ   SEQUENCE   236 AA;  26622 MW;  E7688CB9071A872A CRC64;

  Query Match           40.1%;  Score 556;  DB 1;  Length 236;
  Best Local Similarity  43.4%;  Pred. No. 1.27e-98;
  Matches   72;  Conservative   45;  Mismatches  43;  Indels   6;  Gaps   4;

Db      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| ||| :  |:  ||: :|  ||: :||  |
Qy      88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
             |||  ::   | | : :| :: |::: |: :|| :|:||::: |
Qy     148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT   11
ID   BCL2_HUMAN     STANDARD;      PRT;   239 AA.
AC   P10415; P10416; Q16197; Q13842;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 86259760.
RA   Tsujimoto Y., Croce C.M.;
RT   "Analysis of the structure, transcripts, and protein products of
RT   bcl-2, the gene involved in human follicular lymphoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN   [2]
RP   REVISIONS TO 96; 110 AND 237.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87002488.
RA   Cleary M.L., Smith S.D., Sklar J.;
RT   "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT   2/immunoglobulin transcript resulting from the t(14;18)
RT   translocation.";
RL   Cell 47:19-28(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 88196071.
RA   Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA   Goldman P., Korsmeyer S.J.;
RT   "Alternative promoters and exons, somatic mutation and deregulation
RT   of the Bcl-2-Ig fusion gene in lymphoma.";
RL   EMBO J. 7:123-131(1988).
RN   [5]
RP   SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA.
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DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;

  Query Match           44.2%;  Score 613;  DB 1;  Length 233;
  Best Local Similarity  51.7%;  Pred. No. 4.92e-112;
  Matches    75;  Conservative   35;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: | ::|
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTLAGVVLLGSL 229
           : :|  | | :: : ::| | ||:|
Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    9
ID   BCL2_CHICK     STANDARD;      PRT;   233 AA.
AC   Q00709;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92375724.
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92379084.
RA   Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT   "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT   homologue of the Bcl-2 oncoprotein.";
RL   Biochim. Biophys. Acta 1132:109-113(1992).
CC   -!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
CC       ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
CC       VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
CC       BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
CC       PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
CC       ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
CC       GENERATION SUCH AS MITOCHONDRIA (BY SIMILARITY).
CC   -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
CC       BAK PROTEINS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND
CC       BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
CC       WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D11382; BAA01978.1; -.
DR   EMBL; D11381; BAA01978.1; JOINED.
DR   EMBL; Z11961; CAA78018.1; -.
DR   PIR; A37332; A37332.
DR   PIR; S24390; S24390.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       87    101       BH3.
FT   DOMAIN      130    149       BH1.
FT   DOMAIN      181    196       BH2.
FT   TRANSMEM    208    228       POTENTIAL.
FT   CONFLICT     64     64       E -> S (IN REF. 2).
FT   CONFLICT     67     82       GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
FT                                (IN REF. 2).
FT   CONFLICT    121    121       H -> T (IN REF. 2).
FT   CONFLICT    139    139       G -> V (IN REF. 2).
SQ   SEQUENCE   233 AA;  25687 MW;  5252555ACB6E4C3D CRC64;

  Query Match           40.5%;  Score 561;  DB 1;  Length 233;
  Best Local Similarity  40.5%;  Pred. No. 8.52e-100;
  Matches    79;  Conservative   47;  Mismatches  61;  Indels   8;  Gaps   5;

Db      43 PAPAAAPAAVAAAGASSHHRPEPPGSAAASEVPPAEGLRPAPPGVHLALRQAGDEFSRRY 102
           |:||::| : |  :     |    |   ::   |:||  :| | :| |:| ||||  |:
Qy       2 PTPASTPDTRALVADFVGYRLRQKGYVCGAG--PGEG-PAADP-LHQAMRAAGDEFETRF 57

Db     103 QRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSP 162
           :| |:::::|||:|| :|: ||  | :|||: | ||||:|||| ||: :| ||||:|| |
Qy      58 RRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEP 117

Db     163 LVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN-SM---RPLFDFSWISLKTILSLV 218
           ||  :  |:  ||: :| :|||: :|||  |  |||: ::   | | : :|     : : |
Qy     118 LVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAV 177

Db     219 LVGACITLGAYLGHK 233
           :|| :|:||::: |
Qy     178 ALGALVTVGAFFASK 192


RESULT   10
ID   BCL2_RAT       STANDARD;      PRT;   236 AA.
AC   P49950; Q62837; Q64032;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-2.
GN   BCL2 OR BCL-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
          ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: | ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :| | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    7
ID    BCLX_CHICK      STANDARD;       PRT;   229 AA.
AC    Q07816; Q98908;
DT    01-FEB-1995 (Rel. 31, Created)
DT    01-NOV-1997 (Rel. 35, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    APOPTOSIS REGULATOR BCL-X.
GN    BCL2L1 OR BCLX OR BCL-X.
OS    Gallus gallus (Chicken).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC    Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN    [1]
RP    SEQUENCE FROM N.A. (SHORT FORM).
RX    MEDLINE; 93364977.
RA    Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA    Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT    "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT    of apoptotic cell death.";
RL    Cell 74:597-608(1993).
RN    [2]
RP    SEQUENCE FROM N.A. (LONG FORM).
RC    STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=TESTIS;
RX    MEDLINE; 97264485.
RA    Vilagrasa X., Mezquita C., Mezquita J.;
RT    "Differential expression of bcl-2 and bcl-x during chicken
RT    spermatogenesis.";
RL    Mol. Reprod. Dev. 47:26-29(1997).
CC    -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC        FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC        ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC    -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC        ENVELOPE (BY SIMILARITY).
CC    -!- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT
CC        ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC    -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC        DEVELOPMENT.
CC    -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC        FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC        APOPTOTIC ACTIVITY (BY SIMILARITY).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC    -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC    ----------------------------------------------------------------------
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CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC    or send an email to license@isb-sib.ch).
CC    ----------------------------------------------------------------------
DR    EMBL; Z23110; CAA80657.1; -.
DR    EMBL; U26645; AAB07677.1; -.
DR    PIR; A47537; A47537.
DR    HSSP; P53563; 1AF3.
DR    PROSITE; PS50062; BCL2_FAMILY; 1.
DR    PROSITE; PS01080; BH1; 1.
DR    PROSITE; PS01258; BH2; 1.
DR    PROSITE; PS01259; BH3; 1.
DR    PROSITE; PS01260; BH4_1; 1.
DR    PROSITE; PS50063; BH4_2; 1.
DR    PFAM; PF00452; Bcl-2; 1.
KW    Apoptosis; Transmembrane; Alternative splicing.
FT    DOMAIN        4     24       BH4.
FT    DOMAIN       82     96       BH3.
FT    DOMAIN      125    144       BH1.
FT    DOMAIN      176    191       BH2.
FT    TRANSMEM    206    223       POTENTIAL.
FT    VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                 LSRK -> VRTALP (IN SHORT ISOFORM).
SQ    SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;

  Query Match           44.7%;  Score 620;  DB 1;  Length 229;
  Best Local Similarity 51.7%;  Pred. No. 1.09e-113;
  Matches   77;  Conservative   33;  Mismatches  36;  Indels   3;  Gaps   3;

Db     79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
          |  ::||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||
Qy     39 ADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVA 98

Db    139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWERFVDLYGNNAAAE 198
          || ||:||| |||:||| |||::  |: :|| :| ||: :||| | |||: | :
Qy     99 FFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALED 158

Db    199 LRKGQETFNKWLLTGATVAGVLLLGSLLS 227
           |: :|  | | :: : |:| : ||:|::
Qy    159 ARRLREG-N-WAVS-TVVTGAVALGALVT 184


RESULT    8
ID    BCLX_PIG        STANDARD;       PRT;   233 AA.
AC    O77737;
DT    15-JUL-1999 (Rel. 38, Created)
DT    15-JUL-1999 (Rel. 38, Last sequence update)
DT    15-JUL-1999 (Rel. 38, Last annotation update)
DE    APOPTOSIS REGULATOR BCL-X.
GN    BCL2L1 OR BLC2L OR BCLX.
OS    Sus scrofa (Pig).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC    Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT    "Expression of apoptosis-associated genes in hibernating and stunned
RT    myocardium of pig.";
RL    Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC    -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC        FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
CC        THE BETA ISOFORMS PROMOTE APOPTOSIS.
CC    -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC        BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC        BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC        SIMILARITY).
CC    -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC        ENVELOPE (BY SIMILARITY).
CC    -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC        FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC        APOPTOTIC ACTIVITY (BY SIMILARITY).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC    -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC    -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC    ----------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    ----------------------------------------------------------------------
DR    EMBL; AJ001203; CAA04597.1; -.
DR    PROSITE; PS50062; BCL2_FAMILY; 1.
DR    PROSITE; PS01080; BH1; 1.
DR    PROSITE; PS01258; BH2; 1.
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SQ   SEQUENCE   233 AA;  26049 MW;  E09D3CDD851AE9BE CRC64;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 2.13e-114;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db    85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
        :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy    41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db   145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||::  |: :||: :|  ||: :|||  |  |||: |  ::|
Qy   101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db   205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy   161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    6
ID   BCLX_MOUSE     STANDARD;      PRT;   233 AA.
AC   Q64373; Q60657; Q60658; Q61338;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2A4B;
RA   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
RC   STRAIN=C57BL/6; TISSUE=BRAIN;
RX   MEDLINE; 95331139.
RA   Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
RA   Thompson C.B., Nunez G.;
RT   "bcl-XL is the major bcl-x mRNA form expressed during murine
RT   development and its product localizes to mitochondria.";
RL   Development 120:3033-3042(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
RC   TISSUE=PRE-B CELL;
RX   MEDLINE; 95052604.
RA   Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT   "Cloning and molecular characterization of mouse bcl-x in B and T
RT   lymphocytes.";
RL   J. Immunol. 153:4388-4398(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (BETA ISOFORM).
RC   STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97289584.
RA   Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA   Ohta S., Seldin M.F., Nunez G.;
RT   "Genomic organization, promoter region analysis, and chromosome
RT   localization of the mouse bcl-x gene.";
RL   J. Immunol. 158:4750-4757(1997).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY,
CC       WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC   -!- ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-
CC       X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC       BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC       TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC       ACTIVATED.
CC   -!- DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND
CC       POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC       POSTNATAL TISSUES.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X83574; CAA58557.1; -.
DR   EMBL; L35049; AAA51039.1; -.
DR   EMBL; L35048; AAA51040.1; -.
DR   EMBL; U10102; AAA82174.1; -.
DR   EMBL; U10101; AAA82173.1; -.
DR   EMBL; U10100; AAA82172.1; -.
DR   EMBL; U51279; AAC53460.1; -.
DR   EMBL; U78031; AAB96881.1; -.
DR   EMBL; U78030; AAB96881.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; BCL2L.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
FT                                BCL-X-BETA).
FT   VARSPLIC    194    233       LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
FT                                -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
FT                                X(DELTA-TM)).
SQ   SEQUENCE   233 AA;  26132 MW;  24D2AC79887E072E CRC64;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 2.13e-114;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db    85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
        :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy    41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db   145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
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FT   CONFLICT     81     81       I -> L (IN REF. 4).
FT   CONFLICT    119    119       A -> V (IN REF. 4).
FT   CONFLICT    143    144       FF -> SS (IN REF. 4).
FT   CONFLICT    199    199       A -> T (IN REF. 4).
FT   CONFLICT    201    201       A -> P (IN REF. 4).
SQ   SEQUENCE   233 AA;  26158 MW;  2B62B6C63864BC8F CRC64;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 2.13e-114;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:|||| 
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
            ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: |  ::|
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | | :: : |:| | ||:|
Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    5
ID   BCLX_HUMAN     STANDARD;      PRT;   233 AA.
AC   Q07817; Q92976;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RX   MEDLINE; 93364977.
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (BETA ISOFORM).
RA   Inohara N., Ohta S.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX   MEDLINE; 95372373.
RA   Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA   Korsmeyer S.J.;
RT   "Multiple Bcl-2 family members demonstrate selective dimerizations
RT   with Bax.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN   [4]
RP   MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX   MEDLINE; 96170038.
RA   Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA   Korsmeyer S.J.;
RT   "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL   Nature 379:554-556(1996).
RN   [5]
RP   STRUCTURE BY NMR OF 1-209.
RX   MEDLINE; 97172562.
RA   Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA   Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA   Thompson C.B., Fesik S.W.;
RT   "Structure of Bcl-xL-Bak peptide complex: recognition between
RT   regulators of apoptosis.";
RL   Science 275:983-986(1997).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX   MEDLINE; 96256675.
RA   Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA   Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA   Ng S.L., Fesik S.W.;
RT   "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
RT   cell death.";
RL   Nature 381:335-341(1996).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC       ISOFORM PROMOTES APOPTOSIS.
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCX-X(L) (SHOWN HERE),
CC       BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC       THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC       LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC       LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Z23116; CAA80662.1; -.
DR   EMBL; Z23115; CAA80661.1; -.
DR   EMBL; U72398; AAB17354.1; -.
DR   PDB; 1BXL; 29-OCT-97.
DR   PDB; 1LXL; 21-APR-97.
DR   PDB; 1MAZ; 21-APR-97.
DR   MIM; 600039; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
FT                                VGDVDS (IN ISOFORM BCL-X(BETA)).
FT   MUTAGEN     131    133       FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     135    137       VNW->AIL: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN     138    140       GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN     138    138       G->A: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     148    148       G->E: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN     188    189       WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT                                BY ABOUT HALF.
FT   CONFLICT     70     70       G -> A (IN CAA80661).
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CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       POTENTIAL.
SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;

  Query Match           64.9%;  Score 900;  DB 1;  Length 228;
  Best Local Similarity  66.3%;  Pred. No. 9.34e-181;
  Matches   122;  Conservative   36;  Mismatches  22;  Indels   4;  Gaps   3;

Db      48 SRALVEDLVRYKLCQRSLV--PEPS-GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
           :|||| |:| |:| |:: |  : |: |:|: :|| |||||||||| |||::||::::|:|
Qy      10 TRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69

Db     105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
           ||||:|  ||::|:  ||||| ||||:||||||||||||||||| ||: ::|||:|:|
Qy      70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAY 129

Db     165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
           ||| | |||:|:||| | :|||||:|:||| |||||| : ||:|||||||||:||||:
Qy     130 LETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALGALVTVGAF 188

Db     225 FASK 228
           ||||
Qy     189 FASK 192


RESULT    4
ID   BCLX_RAT       STANDARD;      PRT;   233 AA.
AC   P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-X.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RC   TISSUE=BRAIN;
RA   Michaelidis T.M.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
RC   TISSUE=THYMUS;
RX   MEDLINE; 96278736.
RA   Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT   "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT   unspliced RNA, promotes apoptosis in promyeloid cells.";
RL   J. Biol. Chem. 271:13258-13265(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY;
RX   MEDLINE; 95129487.
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
CC       THE BETA ISOFORMS PROMOTE APOPTOSIS.
CC   -!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
CC       BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
CC       BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
CC       BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC       SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC       OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC       DETECTABLE LEVEL OF BCL-X(S).
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82537; CAA57886.1; -.
DR   EMBL; X82537; CAA57887.1; -.
DR   EMBL; U10579; AAA19257.1; -.
DR   EMBL; U72350; AAB17353.1; -.
DR   EMBL; U72349; AAB17352.1; -.
DR   EMBL; U34963; AAA77686.1; -.
DR   EMBL; S76513; AAC60701.1; ALT_INIT.
DR   EMBL; S78284; AAC60702.1; -.
DR   PDB; 1AF3; 07-JUL-97.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
FT                                IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
FT   CONFLICT      6      6       R -> Q (IN REF. 1).
FT   CONFLICT     12     12       F -> S (IN REF. 2).
FT   CONFLICT     64     64       A -> E (IN REF. 2).
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DR   EMBL; AF030769; AAB86430.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:108052; BCL2L2.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;

  Query Match           97.0%;  Score 1345;  DB 1;  Length 193;
  Best Local Similarity  95.9%;  Pred. No. 1.76e-289;
  Matches   185;  Conservative    6;  Mismatches   1;  Indels   1;  Gaps   1;

Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          |:||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||||:||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    180 GALVTVGAFFASK 192


RESULT    2
ID   BCLW_HUMAN     STANDARD;      PRT;   193 AA.
AC   Q92843;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR BCL-W (KIAA0271).
GN   BCL2L2 OR BCLW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96358615.
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 97191544.
RA   Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. VI.
RT   The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT   analysis of cDNA clones from cell line KG-1 and brain.";
RL   DNA Res. 3:321-329(1996).
CC   -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC       IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC       AND SALIVARY GLAND.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U59747; AAB09055.1; -.
DR   EMBL; D87461; BAA19666.1; -.
DR   HSSP; P53563; 1AF3.
DR   MIM; 601931; -.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;

  Query Match           96.8%;  Score 1341;  DB 1;  Length 193;
  Best Local Similarity  94.8%;  Pred. No. 1.70e-288;
  Matches   183;  Conservative    8;  Mismatches   1;  Indels   1;  Gaps   1;

Db      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
          |:||||:||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
          |||:|:||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
          |||||||||||||
Qy    180 GALVTVGAFFASK 192


RESULT    3
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   APOPTOSIS REGULATOR R1 (XR1) (FRAGMENT).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC   Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEAD;
RX   MEDLINE; 95331613.
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:18:44 2000; MasPar time 8.06 Seconds
725.519 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFVGY.....VTGAVALGALVTVGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 45.917; Variance 78.366; scale 0.586

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1345	97.0	193	1	BCLW_MOUSE	APOPTOSIS REGULATOR BC	1.76e-289
2	1341	96.8	193	1	BCLW_HUMAN	APOPTOSIS REGULATOR BC	1.70e-288
3	900	64.9	228	1	AR1_XENLA	APOPTOSIS REGULATOR R1	9.34e-181
4	623	44.9	233	1	BCLX_RAT	APOPTOSIS REGULATOR BC	2.13e-114
5	623	44.9	233	1	BCLX_HUMAN	APOPTOSIS REGULATOR BC	2.13e-114
6	623	44.9	233	1	BCLX_MOUSE	APOPTOSIS REGULATOR BC	2.13e-114
7	620	44.7	229	1	BCLX_CHICK	APOPTOSIS REGULATOR BC	1.09e-113
8	613	44.2	233	1	BCLX_PIG	APOPTOSIS REGULATOR BC	4.92e-112
9	561	40.5	233	1	BCL2_CHICK	APOPTOSIS REGULATOR BC	8.52e-100
10	556	40.1	236	1	BCL2_RAT	APOPTOSIS REGULATOR BC	1.27e-98
11	556	40.1	239	1	BCL2_HUMAN	APOPTOSIS REGULATOR BC	1.27e-98
12	554	40.0	236	1	BCL2_MOUSE	APOPTOSIS REGULATOR BC	3.72e-98
13	546	39.4	204	1	AR11_XENLA	APOPTOSIS REGULATOR R1	2.78e-96
14	235	17.0	211	1	BAK_HUMAN	BCL-2 HOMOLOGOUS ANTAG	1.42e-26
15	234	16.9	211	1	BAK2_HUMAN	BCL-2 HOMOLOGOUS ANTAG	2.28e-26
16	229	16.5	192	1	BAXA_RAT	APOPTOSIS REGULATOR BA	2.45e-25
17	229	16.5	192	1	BAXA_MOUSE	APOPTOSIS REGULATOR BA	2.45e-25
18	227	16.4	192	1	BAXA_BOVIN	APOPTOSIS REGULATOR BA	6.32e-25
19	226	16.3	143	1	BAXD_HUMAN	BAX PROTEIN, CYTOPLASM	1.01e-24
20	226	16.3	192	1	BAXA_HUMAN	APOPTOSIS REGULATOR BA	1.01e-24
21	215	15.5	218	1	BAXB_HUMAN	APOPTOSIS REGULATOR BA	1.77e-22
22	214	15.4	208	1	BAK_MOUSE	BCL-2 HOMOLOGOUS ANTAG	2.83e-22
23	195	14.1	177	1	NR13_COTJA	APOPTOSIS REGULATOR NR	1.78e-18
24	167	12.0	172	1	BFL1_MOUSE	BCL2-RELATED PROTEIN A	4.51e-13
25	165	11.9	280	1	CED9_CAEEL	APOPTOSIS REGULATOR CE	1.07e-12
26	162	11.7	271	1	CED9_CAEBR	APOPTOSIS REGULATOR CE	3.88e-12
27	159	11.5	175	1	BFL1_HUMAN	BCL2-RELATED PROTEIN A	1.40e-11
28	160	11.5	350	1	MCL1_HUMAN	INDUCED MYELOID LEUKEM	9.12e-12
29	134	9.7	179	1	EAR_ASFE4	APOPTOSIS REGULATOR BC	4.10e-07
30	133	9.6	179	1	EAR_ASFM2	APOPTOSIS REGULATOR BC	6.09e-07
31	133	9.6	179	1	EAR_ASFB7	APOPTOSIS REGULATOR BC	6.09e-07
32	105	7.6	581	1	IRR_RAT	INSULIN RECEPTOR-RELAT	2.03e-02
33	102	7.4	680	1	NOLO_RHISN	NODULATION PROTEIN NOL	5.67e-02
34	99	7.1	421	1	EXG_YARLI	GLUCAN 1,3-BETA-GLUCOS	1.55e-01
35	95	6.9	372	1	LIGC_TRAVE	LIGNINASE C PRECURSOR	5.73e-01
36	95	6.9	647	1	NANH_MICVI	SIALIDASE PRECURSOR (E	5.73e-01
37	95	6.9	843	1	PULA_THEMA	PULLULANASE PRECURSOR	5.73e-01
38	94	6.8	522	1	GAG_HV2G1	GAG POLYPROTEIN [CONTA	7.89e-01
39	94	6.8	1712	1	TGFB_RAT	LATENT TRANSFORMING GR	7.89e-01
40	93	6.7	603	1	GLMS_THETH	GLUCOSAMINE--FRUCTOSE-	1.08e+00
41	92	6.6	262	1	NODJ_BRAJA	NODULATION PROTEIN J.	1.49e+00
42	91	6.6	337	1	TAL1_MOUSE	TRANSALDOLASE (EC 2.2.	2.03e+00
43	91	6.6	337	1	TAL1_HUMAN	TRANSALDOLASE (EC 2.2.	2.03e+00
44	91	6.6	479	1	PGKC_LEIME	PHOSPHOGLYCERATE KINAS	2.03e+00
45	91	6.6	520	1	YBB9_YEAST	HYPOTHETICAL 59.4 KD P	2.03e+00

ALIGNMENTS

RESULT 1
ID BCLW_MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE APOPTOSIS REGULATOR BCL-W.
GN BCL2L2 OR BCLW.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96358615.
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10J;
RX MEDLINE; 98160183.
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC AND SALIVARY GLAND.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION.
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U59746; AAB09056.1; -.

```
Qy    161 R 161


RESULT   14
ENTRY            D37332     #type complete
TITLE            transforming protein (bcl-2-beta) - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                   23-Feb-1997
ACCESSIONS       D37332
REFERENCE        A37332
   #authors      Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal      Nucleic Acids Res. (1992) 20:4187-4192
   #title        Isolation and characterization of the chicken bcl-2 gene:
                   expression in a variety of tissues including lymphoid and
                   neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession    D37332
      ##status        preliminary; nucleic acid sequence not shown; not
                       compared with conceptual translation
      ##molecule_type DNA
      ##residues      1-206 ##label EGU
CLASSIFICATION   #superfamily bcl transforming protein
KEYWORDS         mitochondrion
SUMMARY          #length 206  #molecular-weight 22440  #checksum 5581

  Query Match           36.3%;  Score 503;  DB 2;  Length 206;
  Best Local Similarity  48.7%;  Pred. No. 4.22e-76;
  Matches    56;  Conservative   30;  Mismatches  29;  Indels   0;  Gaps   0;

Db     82 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 141
          :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    142 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 196
          | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||
Qy     90 GPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGW 144


RESULT   15
ENTRY            TVMSB1     #type complete
TITLE            transforming protein bcl-2-beta - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                   18-Jun-1999
ACCESSIONS       B25960
REFERENCE        A90893
   #authors      Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                   C.M.
   #journal      Cell (1987) 49:455-463
   #title        Molecular analysis of mbcl-2: structure and expression of the
                   murine gene homologous to the human gene involved in
                   follicular lymphoma.
   #cross-references MUID:87187643
   #accession    B25960
      ##molecule_type DNA
      ##residues      1-199 ##label NEG
      ##cross-references GB:M16506; NID:g468335; PIDN:AAA37281.1; PID:g387110
GENETICS
   #gene         BCL2
CLASSIFICATION   #superfamily bcl transforming protein
KEYWORDS         alternative splicing; transforming protein
SUMMARY          #length 199  #molecular-weight 22299  #checksum 7397

  Query Match           36.1%;  Score 501;  DB 1;  Length 199;
  Best Local Similarity  48.7%;  Pred. No. 1.09e-75;
  Matches    57;  Conservative   29;  Mismatches  31;  Indels   0;  Gaps   0;

Db     76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
          |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy     28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db    136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 192
          : | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||
Qy     88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGW 144


Search completed: Fri Jun 23 14:18:26 2000
Job time : 16 secs.
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   #cross-references MUID:92375724
   #accession    E37332
      ##status        preliminary; nucleic acid sequence not shown; not
                        compared with conceptual translation
      ##molecule_type DNA
      ##residues      1-33,'E',34-220,'AL',223-236 ##label EGU
GENETICS
   #gene          BCL2
   #introns       192/3
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          alternative splicing; mitochondrion; transforming protein;
                    transmembrane protein
SUMMARY           #length 236  #molecular-weight 26524  #checksum 6709

  Query Match           39.1%;  Score 542;  DB 1;  Length 236;
  Best Local Similarity  42.8%;  Pred. No. 3.92e-84;
  Matches    71;  Conservative   45;  Mismatches  44;  Indels   6;  Gaps   4;

Db      76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLP-WVGACITLGAYLGHK 236
             |||  ::   | | : :| :: |::: :  :|| :|:||::: |
Qy     148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT   11
ENTRY             S24390     #type complete
TITLE             transforming protein (Bcl-2) homolog - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                    16-Jul-1999
ACCESSIONS        S24390
REFERENCE         S24390
   #authors       Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
   #journal       Biochim. Biophys. Acta (1992) 1132:109-113
   #title         Molecular cloning and DNA sequence analysis of cDNA encoding
                    chicken homologue of the Bcl-2 oncoprotein.
   #cross-references MUID:92379084
   #accession    S24390
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-232 ##label CAZ
      ##cross-references EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          mitochondrion; transmembrane protein
SUMMARY           #length 232  #molecular-weight 25839  #checksum 1516

  Query Match           39.0%;  Score 540;  DB 2;  Length 232;
  Best Local Similarity  44.3%;  Pred. No. 1.01e-83;
  Matches    70;  Conservative   37;  Mismatches  46;  Indels   5;  Gaps   3;

Db      79 GCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEELFRDGVNWV 138
           | || | :| |:| ||||  |::| |:::::|||:|| :|  ||  | :|||: | ||
Qy      36 GPAADP-LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94

Db     139 RIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN- 197
           |:|||| ||: :| ||||:|| |||  :  |:  ||: :| :||: :|||  |  |||:
Qy      95 RLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDG 154

Db     198 SM---RPLFDFSWISLKTILSLVLVGACITLGAYLGHK 232
           ::   | | : :|     : : | :|| :|:||::: |
Qy     155 ALEDARRLREGNWAVSTVVTGAVALGALVTVGAFFASK 192


RESULT   12
ENTRY             A47537     #type complete
TITLE             apoptosis regulator bcl-x - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              03-May-1994 #sequence_revision 03-May-1994 #text_change
                    16-Jul-1999
ACCESSIONS        A47537
REFERENCE         A47537
   #authors       Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
                    Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                    C.B.
   #journal       Cell (1993) 74:597-608
   #title         bcl-x, a bcl-2-related gene that functions as a dominant
                    regulator of apoptotic cell death.
   #cross-references MUID:93364977
   #accession    A47537
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-190 ##label BOI
      ##cross-references GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1;
                          PID:g510899
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 190  #molecular-weight 21467  #checksum 5509

  Query Match           38.6%;  Score 535;  DB 2;  Length 190;
  Best Local Similarity  58.9%;  Pred. No. 1.09e-82;
  Matches    66;  Conservative   21;  Mismatches  24;  Indels   1;  Gaps   1;

Db      79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
           |  ::||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||
Qy      39 ADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVA 98

Db     139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWVR-TAL 189
           || ||:||| |||:||| |||::  |: :||  :|  ||: :|||   |||
Qy      99 FFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTAL 150


RESULT   13
ENTRY             JE0203     #type complete
TITLE             apoptosis regulator bcl-x isoform - human
ALTERNATE_NAMES   h-bcl-xbeta
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
                    16-Jul-1999
ACCESSIONS        JE0203
REFERENCE         JE0203
   #authors       Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
                    E.
   #journal       Biochem. Biophys. Res. Commun. (1998) 248:147-152
   #title         Identification of a human cDNA encoding a novel bcl-x
                    isoform.
   #cross-references MUID:98340865
   #accession    JE0203
      ##molecule_type mRNA
      ##residues      1-227 ##label BAN
      ##cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1;
                          PID:g1622941
GENETICS
   #gene          bcl-x
   #map_position 20
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 227  #molecular-weight 25290  #checksum 864

  Query Match           38.6%;  Score 535;  DB 2;  Length 227;
  Best Local Similarity  52.9%;  Pred. No. 1.09e-82;
  Matches    64;  Conservative   28;  Mismatches  29;  Indels   0;  Gaps   0;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWVRTKPLVCPFSLASGQ 204
            ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||    :|   :|  ::
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 R 205
```

```
RESULT    7
ENTRY             I67432     #type fragment
TITLE             BCL-2 - rat (fragment)
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I67432
REFERENCE         I53295
   #authors       Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
   #journal       Endocrinology (1995) 136:232-241
   #title         Expression of members of the bcl-2 gene family in the
                    immature rat ovary: equine chorionic gonadotropin-mediated
                    inhibition of granulosa cell apoptosis is associated with
                    decreased bax and constitutive bcl-2 and bcl-xlong
                    messenger ribonucleic acid levels.
   #cross-references MUID:95129487
   #accession     I67432
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-236 ##label RES
      ##cross-references EMBL:U34964; NID:g1004378; PIDN:AAA77687.1;
                          PID:g1004379
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 236  #checksum 9134

  Query Match           39.8%;  Score 551;  DB 2;  Length 236;
  Best Local Similarity  43.4%;  Pred. No. 5.40e-86;
  Matches    72;  Conservative    45;  Mismatches  43;  Indels   6;  Gaps   4;

Db      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147

Db     196 VELYGP-SM---RPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
             |||  ::   | | : :| :: |::: |: :|| :|:||::: |
Qy     148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT    8
ENTRY             I53744     #type complete
TITLE             gene bcl-2 protein - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              29-May-1998 #sequence_revision 29-May-1998 #text_change
                    16-Jul-1999
ACCESSIONS        I53744
REFERENCE         I53744
   #authors       Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
   #journal       Gene (1994) 140:291-292
   #title         Cloning and sequencing of a cDNA encoding the rat Bcl-2
                    protein.
   #cross-references MUID:94193015
   #accession     I53744
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-236 ##label RES
      ##cross-references GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
GENETICS
   #gene          bcl-2
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 236  #molecular-weight 26550  #checksum 8001

  Query Match           39.6%;  Score 549;  DB 2;  Length 236;
  Best Local Similarity  42.8%;  Pred. No. 1.40e-85;
  Matches    71;  Conservative    45;  Mismatches  44;  Indels   6;  Gaps   4;

Db      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
           |  |||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||
Qy      28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87

Db     136 RDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
           : | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||  |
Qy      88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147

Db     196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
             |||  ::   | | : :| :: |::: |: :|| :|:||::: |
Qy     148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192


RESULT    9
ENTRY             I49057     #type complete
TITLE             bcl-x transmembrane deleted - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I49057
REFERENCE         I49055
   #authors       Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
   #journal       J. Immunol. (1994) 153:4388-4398
   #title         Cloning and molecular characterization of mouse bcl-x in B
                    and T lymphocytes.
   #cross-references MUID:95052604
   #accession     I49057
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-214 ##label RES
      ##cross-references EMBL:U10102; NID:g506649; PIDN:AAA82174.1;
                          PID:g506650
GENETICS
   #gene          bcl-x-long
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 214  #molecular-weight 23900  #checksum 9730

  Query Match           39.1%;  Score 542;  DB 2;  Length 214;
  Best Local Similarity  57.9%;  Pred. No. 3.92e-84;
  Matches    62;  Conservative    24;  Mismatches  21;  Indels   0;  Gaps   0;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:|||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTF 191
           ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||  |
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147


RESULT   10
ENTRY             TVMSA1     #type complete
TITLE             transforming protein bcl-2-alpha - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                    18-Jun-1999
ACCESSIONS        A25960; E37332
REFERENCE         A90893
   #authors       Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                    C.M.
   #journal       Cell (1987) 49:455-463
   #title         Molecular analysis of mbcl-2: structure and expression of the
                    murine gene homologous to the human gene involved in
                    follicular lymphoma.
   #cross-references MUID:87187643
   #accession     A25960
      ##molecule_type DNA
      ##residues      1-236 ##label NEG
      ##cross-references GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1;
                          PID:g387109
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
                    neuronal organs in adult and embryo.
```

```
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    5
ENTRY             A37332     #type complete
TITLE             transforming protein (bcl-2-alpha) - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                    23-Feb-1997
ACCESSIONS        A37332; S35453
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
                    neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession     A37332
      ##status          nucleic acid sequence not shown
      ##molecule_type DNA
      ##residues       1-233 ##label EGU
      ##cross-references EMBL:D11381
GENETICS
   #introns       189/3
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          mitochondrion; transforming protein; transmembrane protein
SUMMARY           #length 233  #molecular-weight 25687  #checksum 99

  Query Match           40.5%;  Score 561;  DB 2;  Length 233;
  Best Local Similarity  40.5%;  Pred. No. 4.59e-88;
  Matches    79;  Conservative   47;  Mismatches  61;  Indels   8;  Gaps   5;

Db     43 PAPAAAPAAVAAAGASSHHRPEPPGSAAASEVPPAEGLRPAPPGVHLALRQAGDEFSRRY 102
          |:||::| : |  :     |    |   ::   |:||  :| | :| |:| |||||  |:
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAG--PGEG-PAADP-LHQAMRAAGDEFETRF 57

Db    103 QRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSP 162
          :| |:::::|||:|| :|: ||  | :|||: | ||||:|||| ||: :| ||||:|| |
Qy     58 RRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEP 117

Db    163 LVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN-SM---RPLFDFSWISLKTILSLV 218
          ||  :  |:  ||: :| :||: :|||  |  |||: ::   | | : :|     : : |
Qy    118 LVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAV 177

Db    219 LVGACITLGAYLGHK 233
           :|| :|:||::: |
Qy    178 ALGALVTVGAFFASK 192


RESULT    6
ENTRY             TVHUA1     #type complete
TITLE             transforming protein bcl-2, splice form alpha - human
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change
                    18-Jun-1999
ACCESSIONS        C37332; A29409; S02452; A24428; A27622; B27622
REFERENCE         A37332
   #authors       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
   #journal       Nucleic Acids Res. (1992) 20:4187-4192
   #title         Isolation and characterization of the chicken bcl-2 gene:
                    expression in a variety of tissues including lymphoid and
                    neuronal organs in adult and embryo.
   #cross-references MUID:92375724
   #accession     C37332
      ##status          nucleic acid sequence not shown; not compared with
                         conceptual translation
      ##molecule_type DNA
      ##residues       1-239 ##label EGU
      ##note           this report is a correction
REFERENCE         A29409
   #authors       Tsujimoto, Y.; Croce, C.M.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
   #title         Analysis of the structure, transcripts, and protein products
                    of bcl-2, the gene involved in human follicular lymphoma.
   #cross-references MUID:86259760
   #accession     A29409
      ##molecule_type mRNA
      ##residues       1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
      ##cross-references GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
      ##note           this sequence has been corrected in reference A37332
REFERENCE         S02452
   #authors       Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett,
                    S.; Goldman, P.; Korsmeyer, S.J..
   #journal       EMBO J. (1988) 7:123-131
   #title         Alternative promoters and exons, somatic mutation and
                    deregulation of the Bcl-2--Ig fusion gene in lymphoma.
   #cross-references MUID:88196071
   #accession     S02452
      ##molecule_type mRNA
      ##residues       1-239 ##label SET
REFERENCE         A24428
   #authors       Cleary, M.L.; Smith, S.D.; Sklar, J.
   #journal       Cell (1986) 47:19-28
   #title         Cloning and structural analysis of cDNAs for bcl-2 and a
                    hybrid bcl-2/immunoglobulin transcript resulting from the t
                    (14;18) translocation.
   #cross-references MUID:87002488
   #accession     A24428
      ##molecule_type mRNA
      ##residues       1-58,'T',60-116,'R',118-239 ##label CLE
      ##cross-references GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
REFERENCE         A27622
   #authors       Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.;
                    Wright, J.J.; Bakhshi, A.
   #journal       Oncogene Res. (1988) 2:263-275
   #title         Consequences of the t(14;18) chromosomal translocation in
                    follicular lymphoma: deregulated expression of a chimeric
                    and mutated BCL-2 gene.
   #cross-references MUID:88217344
   #accession     A27622
      ##molecule_type mRNA
      ##residues       1-58,'T',60-239 ##label HUA
   #accession     B27622
      ##molecule_type DNA
      ##residues       1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2
      ##note           the sequence was determined from the germline gene
COMMENT      Constitutive expression of BCL2 following t(14:18) chromosomal
               translocation is typically found in follicular lymphoma.
GENETICS
   #gene          GDB:BCL2
      ##cross-references GDB:119031; OMIM:151430
   #map_position 18q21.3-18q21.3
FUNCTION
   #description   blocks apoptosis in hematopoietic cells
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          alternative splicing; B-cell lymphoma; follicular lymphoma;
                    proto-oncogene; transforming protein; transmembrane protein
SUMMARY           #length 239  #molecular-weight 26266  #checksum 8323

  Query Match           40.1%;  Score 556;  DB 1;  Length 239;
  Best Local Similarity  43.3%;  Pred. No. 4.98e-87;
  Matches    71;  Conservative   46;  Mismatches  41;  Indels   6;  Gaps   4;

Db     81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
          :|||: :| :  :| ::| |||:|  |:|| |:::::|||:|| :|: ||: | :|||:
Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
          | ||||:|||| ||: :| ||||:|| |||  :  |:  ||: :|  ||: :|||  |
Qy     90 GPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149

Db    201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
          |||  ::   | | : :| :: |::: |: :|| :|:||::: |
Qy    150 LYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
```

```
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    2
ENTRY             S51761     #type complete
TITLE             BCL-X protein - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              07-May-1995 #sequence_revision 01-Sep-1995 #text_change
                    16-Jul-1999
ACCESSIONS        S51761; S51762
REFERENCE         S51761
   #authors       Michaelidis, T.M.
   #submission    submitted to the EMBL Data Library, November 1994
   #accession     S51761
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-233 ##label MIC
      ##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
                          PID:g607177
REFERENCE         S51761
   #authors       Michaelidis, T.M.
   #submission    submitted to the EMBL Data Library, November 1994
   #accession     S51762
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-125,189-233 ##label MI2
      ##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1;
                          PID:g607178
GENETICS
   #introns       125/3
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 233  #molecular-weight 26130  #checksum 6378

  Query Match            44.9%;  Score 623;  DB 2;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 5.74e-101;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
          ||:||| |||:|||: ||::: |: :||: :|  ||: :||| |  |||: |  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    3
ENTRY             B47537     #type complete
TITLE             apoptosis regulator bcl-xL - human
ALTERNATE_NAMES   bcl-2-related protein
CONTAINS          apoptosis regulator bcl-xS
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
                    16-Jul-1999
ACCESSIONS        B47537; C47537
REFERENCE         A47537
   #authors       Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
                    Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                    C.B.
   #journal       Cell (1993) 74:597-608
   #title         bcl-x, a bcl-2-related gene that functions as a dominant
                    regulator of apoptotic cell death.
   #cross-references MUID:93364977
   #accession     B47537
      ##status         nucleic acid sequence not shown; translated from
                         GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-233 ##label BOI
      ##cross-references GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
   #accession     C47537
      ##status         nucleic acid sequence not shown; translated from
                         GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-69,'G',71-125,189-233 ##label BO2
      ##cross-references GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
GENETICS
   #gene          GDB:BCL2L
      ##cross-references GDB:228079
CLASSIFICATION    #superfamily bcl transforming protein
KEYWORDS          alternative splicing; apoptosis
FEATURE
   1-233               #product apoptosis regulator bcl-xL #status predicted
                         #label MAT\
   1-125,189-233       #product apoptosis regulator bcl-xS #status predicted
                         #label MA2
SUMMARY           #length 233  #molecular-weight 26063  #checksum 5340

  Query Match            44.9%;  Score 623;  DB 2;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 5.74e-101;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
          ||:||| |||:|||: ||::: |: :||: :|  ||: :||| |  |||: |  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    4
ENTRY             I67431     #type complete
TITLE             BCL-X-Long - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                    16-Jul-1999
ACCESSIONS        I67431
REFERENCE         I53295
   #authors       Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
   #journal       Endocrinology (1995) 136:232-241
   #title         Expression of members of the bcl-2 gene family in the
                    immature rat ovary: equine chorionic gonadotropin-mediated
                    inhibition of granulosa cell apoptosis is associated with
                    decreased bax and constitutive bcl-2 and bcl-xlong
                    messenger ribonucleic acid levels.
   #cross-references MUID:95129487
   #accession     I67431
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-233 ##label RES
      ##cross-references EMBL:U34963; NID:g1004376; PIDN:AAA77686.1;
                          PID:g1004377
CLASSIFICATION    #superfamily bcl transforming protein
SUMMARY           #length 233  #molecular-weight 26122  #checksum 8310

  Query Match            42.2%;  Score 585;  DB 2;  Length 233;
  Best Local Similarity  49.7%;  Pred. No. 4.78e-93;
  Matches    72;  Conservative   35;  Mismatches  35;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFEQVVNELFRDGVNWGRIVASS 144
          :: ||:| |||||| |:||:||||::|||:|||:  | | || :|||: | ||||:||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNTAPESR 204
          ||:||| |||:|||: ||::: |: :||: :|  ||: :||| |  |||: :  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
```

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MPSRCH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:18:10 2000; MasPar time 12.63 Seconds
716.856 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFVGY.....VTGAVALGALVTVGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.905; Variance 86.927; scale 0.517

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	623	44.9	233	2	I49056	bcl-x long - mouse	5.74e-101
2	623	44.9	233	2	S51761	BCL-X protein - rat	5.74e-101
3	623	44.9	233	2	B47537	apoptosis regulator b	5.74e-101
4	585	42.2	233	2	I67431	BCL-X-Long - rat	4.78e-93
5	561	40.5	233	2	A37332	transforming protein	4.59e-88
6	556	40.1	239	1	TVHUA1	transforming protein	4.98e-87
7	551	39.8	236	2	I67432	BCL-2 - rat (fragment	5.40e-86
8	549	39.6	236	2	I53744	gene bcl-2 protein -	1.40e-85
9	542	39.1	214	2	I49057	bcl-x transmembrane d	3.92e-84
10	542	39.1	236	1	TVMSA1	transforming protein	3.92e-84
11	540	39.0	232	2	S24390	transforming protein	1.01e-83
12	535	38.6	190	2	A47537	apoptosis regulator b	1.09e-82
13	535	38.6	227	2	JE0203	apoptosis regulator b	1.09e-82
14	503	36.3	206	2	D37332	transforming protein	4.22e-76
15	501	36.1	199	1	TVMSB1	transforming protein	1.09e-75
16	495	35.7	216	2	B37332	transforming protein	1.85e-74
17	491	35.4	205	1	TVHUB1	transforming protein	1.22e-73
18	404	29.1	154	2	I58194	gene bcl-2 protein -	5.41e-56
19	235	17.0	211	2	S58873	Bak protein - human	2.90e-23
20	234	16.9	211	2	S58875	cdn-2 protein - human	4.43e-23
21	233	16.8	192	2	D47538	bcl-2-associated prot	6.76e-23
22	226	16.3	143	2	I38921	bcl-2-associated prot	1.29e-21
23	226	16.3	192	2	A47538	bcl-2-associated prot	1.29e-21
24	225	16.2	133	2	I53295	bcl-2-associated prot	1.96e-21
25	215	15.5	218	2	B47538	bcl-2-associated prot	1.26e-19
26	205	14.8	170	2	I49055	bcl-x short - mouse	7.78e-18
27	201	14.5	176	2	I67435	gene bcl-xshort prote	3.99e-17
28	195	14.1	177	2	S54778	NR-13 protein - quail	4.55e-16
29	167	12.0	172	2	I49449	hemopoietic-specific	2.92e-11
30	165	11.9	280	2	A53189	apoptosis suppressor	6.31e-11
31	159	11.5	175	2	I39055	Bcl-2 related - human	6.23e-10
32	160	11.5	350	2	A47476	BCL2 homolog MCL1 - h	4.27e-10
33	103	7.4	168	2	T03168	hypothetical protein	1.84e-01
34	100	7.2	630	2	JC5374	angiotensin-convertin	4.58e-01
35	97	7.0	798	2	B71196	probable transitional	1.12e+00
36	97	7.0	1937	2	T03224	probable polyketide s	1.12e+00
37	95	6.9	372	2	S32581	lignin peroxidase (EC	2.01e+00
38	95	6.9	647	2	A45244	exo-alpha-sialidase (	2.01e+00
39	95	6.9	843	2	H72204	pullulanase - Thermot	2.01e+00
40	94	6.8	494	2	C70667	hypothetical protein	2.69e+00
41	94	6.8	522	1	FOLJGG	gag polyprotein - hum	2.69e+00
42	94	6.8	795	2	F75154	cell division control	2.69e+00
43	94	6.8	1712	2	A38261	masking protein precu	2.69e+00
44	94	6.8	3104	2	S20473	fatty-acid synthase (	2.69e+00
45	93	6.7	657	2	E70529	hypothetical protein	3.58e+00

ALIGNMENTS

```
RESULT    1
ENTRY           I49056      #type complete
TITLE           bcl-x long - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                  16-Jul-1999
ACCESSIONS      I49056; S52866
REFERENCE       I49055
  #authors      Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
  #journal      J. Immunol. (1994) 153:4388-4398
  #title        Cloning and molecular characterization of mouse bcl-x in B
                  and T lymphocytes.
  #cross-references MUID:95052604
  #accession    I49056
    ##status       preliminary; translated from GB/EMBL/DDBJ
    ##molecule_type mRNA
    ##residues     1-233 ##label RES
    ##cross-references EMBL:U10101; NID:g506647; PIDN:AAA82173.1;
                      PID:g506648
REFERENCE       S52866
  #authors      Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
  #submission   submitted to the EMBL Data Library, November 1994
  #description  IL-5 inhibits anti-IgM-induced apoptosis in an immature B
                  cell line through inductin of bcl-X1.
  #accession    S52866
    ##status       preliminary
    ##molecule_type mRNA
    ##residues     1-233 ##label KAM
    ##cross-references EMBL:X83574; NID:g695622; PIDN:CAA58557.1;
                      PID:g695623
CLASSIFICATION  #superfamily bcl transforming protein
SUMMARY         #length 233  #molecular-weight 26132  #checksum 5739

  Query Match           44.9%;  Score 623;  DB 2;  Length 233;
  Best Local Similarity 52.4%;  Pred. No. 5.74e-101;
  Matches   76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
          ||:|| |||:|||: ||::: |: :||: :|  ||: :|||  |  |||: |  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
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RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF115380; AAD13295.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   PROSITE; PS01080; BH1; 1.
SQ   SEQUENCE   330 AA;  35195 MW;  CC87F2E0 CRC32;

  Query Match           12.6%;  Score 175;  DB 11;  Length 330;
  Best Local Similarity  24.5%;  Pred. No. 6.35e-14;
  Matches   37;  Conservative   33;  Mismatches  75;  Indels   6;  Gaps   6;

Db    160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
          :::: | ||: :     | | || |:|:    :::|  ||  :     :|  :   | :
Qy     16 DFVG-YRLRQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71

Db    219 NEDDVKSFSRVMTHVFKDGVTNWGRIVTLISFGAFVAKHLKSINQESCIEPLAESITDVL 278
              |::|   :|  |  ||||:|::: ||| :     : : |: :  : : |   |
Qy     72 PGSAQQRFTQVSDELFQGG-PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYL 130

Db    279 VRTKRDWLVKQRGWDGFVEFFHVQDLEGGIR 309
             ||:   ||  |  ::   || : |
Qy    131 ETRLADWIHSSGGWADFTALYGDGALEDARR 161


RESULT   13
ID   Q9W6F1      PRELIMINARY;      PRT;   211 AA.
AC   Q9W6F1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 99190706.
RA   LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
RT   "Role of Nr13 in regulation of programmed cell death in the bursa of
RT   Fabricius.";
RL   Genes Dev. 13:718-728(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SOFER L., BURNSIDE J.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF120210; AAD31644.1; -.
DR   PROSITE; PS01080; BH1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   211 AA;  23143 MW;  DEE4E997 CRC32;

  Query Match           12.1%;  Score 168;  DB 13;  Length 211;
  Best Local Similarity  22.7%;  Pred. No. 1.23e-12;
  Matches   30;  Conservative   31;  Mismatches  70;  Indels   1;  Gaps   1;

Db     55 PGRASSAVMEKALETLRRVGDGVMQKHELAFQGMLRKLEIKKEDDLQAVCEVAAQVFNDG 114
          :| : ::  :   :::|  ||    :   :|  :   | :       |   :|: ::|  |
Qy     31 AGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90

Db    115 VTNWGRVVTLISFGAFVAKHLKSINQEKCITSLAGIITDALVSSKREWLMSQGGWEGFVD 174
            ||||:|::: ||| :     : : |  :  :   |   | :   :|: | |||  |
Qy     91 -PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149

Db    175 FFRVEDLESSIR 186
          ::    || : |
Qy    150 LYGDGALEDARR 161


RESULT   14
ID   O77738      PRELIMINARY;      PRT;    80 AA.
AC   O77738;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BAK PROTEIN (FRAGMENT).
GN   BAK.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ001204; CAA04598.1; -.
DR   HSSP; Q16611; 1BXL.
DR   PROSITE; PS01259; BH3; 1.
DR   PFAM; PF00452; Bcl-2; 1.
KW   Apoptosis.
FT   NON_TER       1      1
FT   NON_TER      80     80
SQ   SEQUENCE   80 AA;  8818 MW;  973BE2D0 CRC32;

  Query Match           10.4%;  Score 144;  DB 6;  Length 80;
  Best Local Similarity  35.4%;  Pred. No. 2.28e-08;
  Matches   17;  Conservative   15;  Mismatches  16;  Indels   0;  Gaps   0;

Db     33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
          ||::: |:   |  :  :|: |: :| : || ::  ||::| ||||:|
Qy     50 GDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLV 97


RESULT   15
ID   O55178      PRELIMINARY;      PRT;   128 AA.
AC   O55178;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN A1C (A1-C PROTEIN).
GN   BCL2A1C OR A1C.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=LIVER;
RA   HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RA   NAKAYAMA K., NAKAYAMA K.-I.;
RL   Int. Immunol. 0:0-0(1998).
DR   EMBL; U23779; AAB97955.1; -.
DR   MGD; MGI:1278327; Bcl2a1c.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   128 AA;  14763 MW;  DF4F2653 CRC32;

  Query Match            8.7%;  Score 120;  DB 11;  Length 128;
  Best Local Similarity  38.1%;  Pred. No. 2.21e-04;
  Matches   16;  Conservative   12;  Mismatches  12;  Indels   2;  Gaps   2;

Db     58 DFHVESIDTTRIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL 99
          ::|| :  :::  | || :  |: |  ||||:|::| ||: |
Qy     67 QLHVTP-GSAQQRFTQVSDELFQGGP-NWGRLVAFFVFGAAL 106


Search completed: Fri Jun 23 14:19:38 2000
Job time : 25 secs.
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RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF051093; AAC61928.1; -.
SQ   SEQUENCE   170 AA;  18729 MW;  79B4BBE6 CRC32;

  Query Match           12.7%;  Score 176;  DB 11;  Length 170;
  Best Local Similarity  25.0%;  Pred. No. 4.14e-14;
  Matches    28;  Conservative   35;  Mismatches  47;  Indels   2;  Gaps   2;

Db      21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
           :|:   |    :| | |:  :|: |:    :|  : :|:::  |:::|   |:: |  ||
Qy      36 GPAADPLHQAMRAAGDEF-ETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94

Db      80 KVVSLYSVAAGLAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 131
           ::|:::  :|:|  : |     ::|  : | :  ::   || |::  |||:|
Qy      95 RLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWAD 146


RESULT    9
ID   O55177      PRELIMINARY;      PRT;   172 AA.
AC   O55177;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN A1B (A1-B PROTEIN).
GN   BCL2A1B OR A1B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=LIVER;
RA   HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RA   NAKAYAMA K., NAKAYAMA K.-I.;
RL   Int. Immunol. 0:0-0(1998).
DR   EMBL; U23778; AAB97954.1; -.
DR   EMBL; U23777; AAB97954.1; JOINED.
DR   MGD; MGI:1278326; Bcl2a1b.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   172 AA;  20048 MW;  FA16DF6C CRC32;

  Query Match           12.6%;  Score 175;  DB 11;  Length 172;
  Best Local Similarity  33.7%;  Pred. No. 6.35e-14;
  Matches    29;  Conservative   20;  Mismatches  30;  Indels   7;  Gaps   5;

Db      58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
           ::|| :  :|:  | || :  |: |  ||||:|::| ||: |    :  |  :| ||
Qy      67 QLHVTP-GSAQQRFTQVSDELFQGGP-NWGRLVAFFVFGAALCAESVNKEMEPL-VG--- 120

Db     117 QVSSFVAEFIINNTGEWIRRNGGWED 142
           ||    :  ::    ::||: :||| |
Qy     121 QVQDWIVAYLETRLADWIHSSGGWAD 146


RESULT   10
ID   O55179      PRELIMINARY;      PRT;   172 AA.
AC   O55179;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN A1D (A1-D PROTEIN).
GN   BCL2A1D OR A1D.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SV; TISSUE=LIVER;
RA   HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
RA   NAKAYAMA K., NAKAYAMA K.-I.;
RL   Int. Immunol. 0:0-0(1998).
DR   EMBL; U23781; AAB97956.1; -.
DR   EMBL; U23780; AAB97956.1; JOINED.
DR   MGD; MGI:1278325; Bcl2a1d.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   172 AA;  20048 MW;  1B340DDD CRC32;

  Query Match           12.6%;  Score 174;  DB 11;  Length 172;
  Best Local Similarity  33.7%;  Pred. No. 9.71e-14;
  Matches    29;  Conservative   20;  Mismatches  30;  Indels   7;  Gaps   5;

Db      58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
           ::|| :  :|:  | || :  |: |  ||||:|::| ||: |    :  |  :| ||
Qy      67 QLHVTP-GSAQQRFTQVSDELFQGGP-NWGRLVAFFVFGAALCAESVNKEMEPL-VG--- 120

Db     117 QVSSFVAEFIMNNTGEWIRRNGGWED 142
           ||    :  ::    ::||: :||| |
Qy     121 QVQDWIVAYLETRLADWIHSSGGWAD 146


RESULT   11
ID   Q9W6F2      PRELIMINARY;      PRT;   174 AA.
AC   Q9W6F2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   PROTEIN A1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 99190706.
RA   LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
RT   "Role of Nr13 in regulation of programmed cell death in the bursa of
RT   Fabricius.";
RL   Genes Dev. 13:718-728(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   SOFER L., BURNSIDE J.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF120211; AAD31645.1; -.
SQ   SEQUENCE   174 AA;  20095 MW;  70F5FDAA CRC32;

  Query Match           12.6%;  Score 174;  DB 13;  Length 174;
  Best Local Similarity  24.4%;  Pred. No. 9.71e-14;
  Matches    30;  Conservative   33;  Mismatches  52;  Indels   8;  Gaps   6;

Db      27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNTNW 86
           |||   : : :|  :  :: :   ::  :  :: :|:     | |  | :| | :|  ||
Qy      36 GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR-FTQVSDELF-QGGPNW 93

Db      87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKEKISYFITEYIINNKAAWIDANGGWENGFL 145
           ||:::::| ||: | :  :      | |:  : |   :: |:    | || ::||| : |
Qy      94 GRLVAFFVFGAALCAESVNKEMEPLVGQVQDWI---VA-YLETRLADWIHSSGGWAD-FT 148

Db     146 TKF 148
           : :
Qy     149 ALY 151


RESULT   12
ID   Q9Z1P3      PRELIMINARY;      PRT;   330 AA.
AC   Q9Z1P3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MCL-1 PROTEIN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LEO C.P., HSU S.Y., HSUEH A.J.W.;
RT   "Sequence of rat Mcl-1, a Bcl-2-related gene.";
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RA   HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF136230; AAD33683.1; -.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
SQ   SEQUENCE   170 AA;  19031 MW;  8B29C9C1 CRC32;

  Query Match           14.9%;  Score 207;  DB 11;  Length 170;
  Best Local Similarity  58.3%;  Pred. No. 5.41e-20;
  Matches   28;  Conservative   11;  Mismatches   8;  Indels   1;  Gaps   1;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
           :: ||:| |||||| |:||:||||::|||:|||:| | | | |  :|:
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVS-DELF 87


RESULT    6
ID   O35425      PRELIMINARY;      PRT;   213 AA.
AC   O35425;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   BCL-2-RELATED OVARIAN KILLER PROTEIN.
GN   BOK OR MTD.
OS   Rattus norvegicus (Rat), and Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, UTERUS;
RX   MEDLINE; 98024143.
RA   HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.W.;
RT   "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT   reproductive tissues and heterodimerizes with selective anti-apoptotic
RT   Bcl-2 family members.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, UTERUS;
RA   HSU S.Y., HSUEH A.J.W.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=MOUSE;
RA   INOHARA N., EKHTERAE D., GARCIA I., CARRIO R., MERINO J., MERRY A.,
RA   CHEN S., NUNEZ G.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF027954; AAB87418.1; -.
DR   EMBL; AF027707; AAC53582.1; -.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   213 AA;  23456 MW;  29761D17 CRC32;

  Query Match           13.1%;  Score 182;  DB 11;  Length 213;
  Best Local Similarity  27.7%;  Pred. No. 3.16e-15;
  Matches   28;  Conservative   31;  Mismatches  37;  Indels   5;  Gaps   5;

Db      75 GDELE-QIRPSVYRNVARQLHIPLQSEPVVTDAFLAVAGHIFSAGITWGKVVSLYSVAAG 133
           |||:| ::| : : ::| |||:   : :   : |  |:  :| :|  ||::|:::  :|:
Qy      50 GDEFETRFRRT-FSDLAAQLHVT-PG-SA-QQRFTQVSDELFQGGPNWGRLVAFFVFGAA 105

Db     134 LAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 174
           |  : |     ::|  : | :  ::   || |::  |||:|
Qy     106 LCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWAD 146


RESULT    7
ID   P97287      PRELIMINARY;      PRT;   331 AA.
AC   P97287;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   EAT/MCL-1 PROTEIN (MCL1).
GN   EAT/MCL-1 OR MCL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98322120.
RA   OKITA H., UMEZAWA A., SUZUKI A., HATA J.;
RT   "Up-regulated expression of murine Mcl1/EAT, a bcl-2 related gene, in
RT   the early stage of differentiation of murine embryonal carcinoma cells
RT   and embryonic stem cells.";
RL   Biochim. Biophys. Acta 1398:335-341(1998).
RN   [2]
RP   SEQUENCE OF 1-65 FROM N.A.
RC   STRAIN=129/SVJ;
RX   MEDLINE; 98336293.
RA   CHAO J.R., WANG J.M., LEE S.F., PENG H.W., LIN Y.H., CHOU C.H.,
RA   LI J.C., HUANG H.M., CHOU C.K., KUO M.L., YEN J.J.Y., YANG-YEN H.F.;
RT   "mcl-1 is an immediate-early gene activated by the granulocyte-
RT   macrophage colony-stimulating factor (GM-CSF) signaling pathway and is
RT   one component of the GM-CSF viability response.";
RL   Mol. Cell. Biol. 18:4883-4898(1998).
DR   EMBL; U35623; AAC31790.1; -.
DR   EMBL; AF063886; AAC27929.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:101769; Mcl1.
DR   PROSITE; PS01080; BH1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   331 AA;  35217 MW;  3103C5FE CRC32;

  Query Match           12.8%;  Score 177;  DB 11;  Length 331;
  Best Local Similarity  25.2%;  Pred. No. 2.70e-14;
  Matches   33;  Conservative   30;  Mismatches  64;  Indels   4;  Gaps   4;

Db     181 GEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIKNEGDVKSFSRVMVHVFKDGVT 240
           || |:|:    :::|  ||  :     :|  :   | :   :    |::|   :|  |
Qy      34 GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG-P 91

Db     241 NWGRIVTLISFGA-FVAKHLKSVNQESFIEPLAETITDVLVRTKRDWLVKQRGWDGFVEF 299
           ||||:|::: ||| : |  ::  : |:::  : : |   |     ||:    ||  |  :
Qy      92 NWGRLVAFFVFGAALCAESVNK-EMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTAL 150

Db     300 FHVQDLEGGIR 310
           :    || : |
Qy     151 YGDGALEDARR 161


RESULT    8
ID   O88857      PRELIMINARY;      PRT;   170 AA.
AC   O88857;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   BCL-2-RELATED OVARIAN KILLER PROTEIN.
GN   BOK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY, UTERUS;
RX   MEDLINE; 98024143.
RA   HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.;
RT   "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
RT   reproductive tissues and heterodimerizes with selective anti-apoptotic
RT   Bcl-2 family members.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY, UTERUS;
RA   HSU S.Y., HSUEH A.J.W.;
RT   "A splicing variant of the Bcl-2 member Bok with a truncated BH3
RT   domain induces apoptosis without dimerization with anti-apoptotic Bcl-
RT   2 proteins.";
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Qy    180 GALVTVGAFFASK 192


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ID   O35844      PRELIMINARY;      PRT;   233 AA.
AC   O35844;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL2-LIKE (BCL-XL).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   YANG X.-F., WEBER G.F., CANTOR H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51278; AAC53459.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl21.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   233 AA;  26033 MW;  A4A14278 CRC32;

  Query Match           46.0%;  Score 638;  DB 11;  Length 233;
  Best Local Similarity  53.1%;  Pred. No. 2.64e-113;
  Matches   77;  Conservative   34;  Mismatches  31;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
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Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGKEGFNRWFLTGMTVAGVVLLGSL 229
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Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT    3
ID   O02718      PRELIMINARY;      PRT;   229 AA.
AC   O02718;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL-2 (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC   Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN; TISSUE=THYMUS;
RA   REYES R.A., COCKERELL G.L.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U92434; AAB53319.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
FT   NON_TER     229    229
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  Best Local Similarity  42.7%;  Pred. No. 1.15e-95;
  Matches   70;  Conservative   48;  Mismatches  40;  Indels   6;  Gaps   4;

Db     71 AAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFRD 130
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Qy     30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89

Db    131 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFVE 190
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Db    191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
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AC   O35843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL2-LIKE (BCL-X-GAMMA).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE; 98051053.
RA   YANG X.-F., WEBER G.F., CANTOR H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51277; AAC53458.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl21.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   235 AA;  26122 MW;  FB0B0207 CRC32;

  Query Match           38.5%;  Score 533;  DB 11;  Length 235;
  Best Local Similarity  58.1%;  Pred. No. 1.32e-89;
  Matches   61;  Conservative   25;  Mismatches  19;  Indels   0;  Gaps   0;

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Db    145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWG 189
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Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWA 145


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AC   Q9WUI5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL-X SHORT.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
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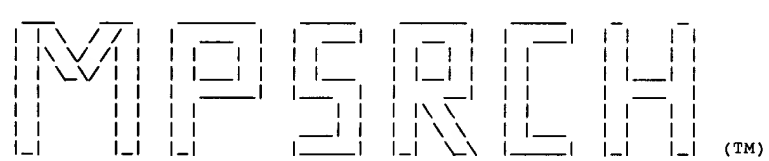

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:19:13 2000; MasPar time 19.74 Seconds
674.404 Million cell updates/sec

Tabular output not generated.

Title: >US-09-155-327B-9
Description: (1-192) from US09155327B.pep
Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFVGY.....VTGAVALGALVTVGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 44.372; Variance 79.166; scale 0.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1343	96.9	193	11	O88996	BCL-W.	3.25e-277
2	638	46.0	233	11	O35844	BCL2-LIKE (BCL-XL).	2.64e-113
3	560	40.4	229	6	O02718	BCL-2 (FRAGMENT).	1.15e-95
4	533	38.5	235	11	O35843	BCL2-LIKE (BCL-X-GAMMA	1.32e-89
5	207	14.9	170	11	Q9WUI5	BCL-X SHORT.	5.41e-20
6	182	13.1	213	11	O35425	BCL-2-RELATED OVARIAN	3.16e-15
7	177	12.8	331	11	P97287	EAT/MCL-1 PROTEIN (MCL	2.70e-14
8	176	12.7	170	11	O88857	BCL-2-RELATED OVARIAN	4.14e-14
9	175	12.6	172	11	O55177	B-CELL LEUKEMIA/LYMPHO	6.35e-14
10	174	12.6	172	11	O55179	B-CELL LEUKEMIA/LYMPHO	9.71e-14
11	174	12.6	174	13	Q9W6F2	PROTEIN A1.	9.71e-14
12	175	12.6	330	11	Q9Z1P3	MCL-1 PROTEIN.	6.35e-14
13	168	12.1	211	13	Q9W6F1	MYELOID CELL LEUKEMIA	1.23e-12
14	144	10.4	80	6	O77738	BAK PROTEIN (FRAGMENT)	2.28e-08
15	120	8.7	128	11	O55178	B-CELL LEUKEMIA/LYMPHO	2.21e-04
16	117	8.4	923	4	Q9Y3R2	NUCLEAR TRANSPORT RECE	6.59e-04
17	103	7.4	168	14	O36423	SIMILAR TO BCL-FAMILY	8.67e-02
18	103	7.4	521	14	Q9YTU1	GAG PROTEIN.	8.67e-02
19	102	7.4	1259	5	O44971	C42C1.4 PROTEIN.	1.21e-01
20	100	7.2	630	5	Q24222	METALLOPEPTIDASE.	2.34e-01
21	99	7.1	175	14	P90504	ORF 16.	3.25e-01
22	98	7.1	187	14	Q9WRT6	BCL-2 HOMOLOG.	4.50e-01
23	98	7.1	975	4	Q9Y5L0	TRANSPORTIN-SR.	4.50e-01
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25	97	7.0	597	14	Q9YUR4	TERMINAL PROTEIN.	6.22e-01
26	97	7.0	798	1	O59515	798AA LONG HYPOTHETICA	6.22e-01
27	97	7.0	967	5	Q18965	D2013.5 PROTEIN.	6.22e-01
28	97	7.0	1937	2	O30482	PKS MODULE 4.	6.22e-01
29	96	6.9	1713	11	O88349	LATENT TGF BETA BINDIN	8.57e-01
30	94	6.8	279	14	O57148	SEROTYPE B PUTATIVE MA	1.62e+00
31	94	6.8	289	2	Q51585	HYPOTHETICAL 32.3 KD P	1.62e+00
32	94	6.8	494	2	P95148	HYPOTHETICAL 53.6 KD P	1.62e+00
33	94	6.8	728	10	O04512	SEQUENCE OF BAC F21M12	1.62e+00
34	94	6.8	757	14	O37361	PUTATIVE RNA DEPENDENT	1.62e+00
35	94	6.8	3104	2	Q04846	FATTY ACID SYNTHASE (E	1.62e+00
36	93	6.7	262	2	Q9Z3I2	NODJ.	2.21e+00
37	93	6.7	440	1	Q9YFI3	440AA LONG HYPOTHETICA	2.21e+00
38	93	6.7	555	4	Q9Y625	GLYPICAN-6.	2.21e+00
39	93	6.7	657	2	O07192	HYPOTHETICAL 70.8 KD P	2.21e+00
40	91	6.6	140	11	P70703	TRANSALDOLASE 1 (EC 2.	4.10e+00
41	91	6.6	337	4	O00751	TRANSALDOLASE (EC 2.2.	4.10e+00
42	92	6.6	413	2	P94131	CIS,CIS-MUCONATE TRANS	3.01e+00
43	91	6.6	505	1	O27209	CONSERVED PROTEIN (FLP	4.10e+00
44	91	6.6	896	1	O30061	MOLYBDOPTERIN OXIDORED	4.10e+00
45	91	6.6	4101	5	O02425	R31.1 PROTEIN.	4.10e+00

ALIGNMENTS

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ID   O88996      PRELIMINARY;      PRT;   193 AA.
AC   O88996;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   BCL-W.
GN   BCL-W.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA   HAMNER S., SKOGLOSA Y., LINDHOLM D.;
RT   "Differential expression of Bcl-w and Bcl-x mRNA in the developing and
RT   adult nervous system.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF096291; AAC64200.1; -.
DR   HSSP; P53563; 1AF3.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PFAM; PF00452; Bcl-2; 1.
SQ   SEQUENCE   193 AA;  20820 MW;  6E5F84BA CRC32;

  Query Match           96.9%;  Score 1343;  DB 11;  Length 193;
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CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/081,448
CC         FILING DATE:  19930622
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  No. 5646008thrup, Thomas E.
CC         REGISTRATION NUMBER:  33,268
CC         REFERENCE/DOCKET NUMBER:  ARCD090
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  312-744-0090
CC         TELEFAX:  312-755-4489
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
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Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   15
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XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 59, Application US/08661479
XX
CC    Sequence 59, Application US/08661479
CC    Patent No. 5834209
CC     GENERAL INFORMATION:
CC       APPLICANT:  KORSMEYER, Stanley J.
CC       TITLE OF INVENTION:  Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC       TITLE OF INVENTION:  REGULATOR
CC       NUMBER OF SEQUENCES:  59
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC         STREET:  379 Lytton Avenue
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  US
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/661,479
CC         FILING DATE:  11-JUN-1995
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/333,565
CC         FILING DATE:  31-OCT-1994
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Smith, William M
CC         REGISTRATION NUMBER:  30,223
CC         REFERENCE/DOCKET NUMBER:  15726A-000700
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 326-2400
CC         TELEFAX:  (415) 326-2422
CC     INFORMATION FOR SEQ ID NO:  59:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  unknown
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SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

  Query Match           44.9%;  Score 623;  DB 2;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


Search completed: Fri Jun 23 14:20:05 2000
Job time : 9 secs.
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CC       TITLE OF INVENTION:  NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
CC       TITLE OF INVENTION:  ENCODING THE PROTEINS AND METHODS OF USE THEREOF
CC       NUMBER OF SEQUENCES:  22
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  MORRISON & FOERSTER
CC         STREET:  755 Page Mill Road
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94304-1018
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
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CC         APPLICATION NUMBER:  US/08/471,057
CC         FILING DATE:
CC         CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/320,157
CC         FILING DATE:  07-OCT-1994
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  LEHNHARDT, SUSAN K.
CC         REGISTRATION NUMBER:  33,943
CC         REFERENCE/DOCKET NUMBER:  23647-20007.20
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 813-5600
CC         TELEFAX:  (415) 494-0792
CC         TELEX:  706141
CC     INFORMATION FOR SEQ ID NO:  14:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  linear
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

  Query Match           44.9%;  Score 623;  DB 3;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches   76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||  |  |||: |  ::|
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | | :: : |:| | ||:|
Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   13
ID   US-08-333-565-59     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 59, Application US/08333565
XX
CC    Sequence 59, Application US/08333565
CC    Patent No. 5622852
CC     GENERAL INFORMATION:
CC       APPLICANT:  KORSMEYER, Stanley J.
CC       TITLE OF INVENTION:  Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
CC       TITLE OF INVENTION:  REGULATOR
CC       NUMBER OF SEQUENCES:  59
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Townsend and Townsend Khourie and Crew
CC         STREET:  379 Lytton Avenue
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  US
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/333,565
CC         FILING DATE:  31-OCT-1994
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Smith, William M
CC         REGISTRATION NUMBER:  30,223
CC         REFERENCE/DOCKET NUMBER:  15726A-000700
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 326-2400
CC         TELEFAX:  (415) 326-2422
CC     INFORMATION FOR SEQ ID NO:  59:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  single
CC         TOPOLOGY:  unknown
CC       MOLECULE TYPE:  peptide
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

  Query Match           44.9%;  Score 623;  DB 1;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches   76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||  |  |||: |  ::|
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | | :: : |:| | ||:|
Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   14
ID   US-08-081-448-6     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 6, Application US/08081448
XX
CC    Sequence 6, Application US/08081448
CC    Patent No. 5646008
CC     GENERAL INFORMATION:
CC       APPLICANT:  Thompson, Craig B.
CC       APPLICANT:  Boise, Lawrence H.
CC       TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
CC       TITLE OF INVENTION:  Compositions and Methods
CC       NUMBER OF SEQUENCES:  8
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Arnold, White & Durkee
CC         STREET:  321 No. 5646008th Clark Street, Suite 800
CC         CITY:  Chicago
CC         STATE:  IL
CC         COUNTRY:  USA
CC         ZIP:  60610
CC       COMPUTER READABLE FORM:
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ID   PCT-US94-07089-7     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 7, Application PC/TUS9407089
XX
CC    Sequence 7, Application PC/TUS9407089
CC     GENERAL INFORMATION:
CC       APPLICANT:
CC       TITLE OF INVENTION:  Vertebrate Apoptosis Gene:
CC       TITLE OF INVENTION:  Compositions and Methods
CC       NUMBER OF SEQUENCES:  9
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Arnold, White & Durkee
CC         STREET:  P.O. Box 4433
CC         CITY:  Houston
CC         STATE:  TX
CC         COUNTRY:  United States of America
CC         ZIP:  77210
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS, ASCII
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US94/07089
CC         FILING DATE:  CONCURRENTLY FILED
CC         CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/081.448
CC         FILING DATE:  22 JUNE 1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  PARKER, David L.
CC         REGISTRATION NUMBER:  32,165
CC         REFERENCE/DOCKET NUMBER:  ARCD090
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  512-320-7200
CC         TELEFAX:  713-789-2679
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26049 MW; 275801 CN;

  Query Match           44.9%;  Score 623;  DB 4;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
          ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||  |  |||: |  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   11
ID   US-08-470-670A-7     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 7, Application US/08470670A
XX
CC    Sequence 7, Application US/08470670A
CC    Patent No. 5834309
CC    Patent No. 5834309 5710045
CC     GENERAL INFORMATION:
CC       APPLICANT:  Thompson, Craig B. B.
CC       APPLICANT:  Boise, Lawrence H.
CC       TITLE OF INVENTION:  VERTEBRATE APOPTOSIS GENE:
CC       TITLE OF INVENTION:  COMPOSITIONS AND METHODS
CC       NUMBER OF SEQUENCES:  18
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Arnold, White & Durkee
CC         STREET:  P.O. Box 4433
CC         CITY:  Houston
CC         STATE:  Texas
CC         COUNTRY:  United States of America
CC         ZIP:  77210
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/470,670A
CC         FILING DATE:
CC         CLASSIFICATION:  514
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/081,448
CC         FILING DATE:  22-JUN-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Highlander, Steven L.
CC         REGISTRATION NUMBER:  37,642
CC         REFERENCE/DOCKET NUMBER:  ARCD:090--1
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (512) 418-3000
CC         TELEFAX:  (512) 474-7577
CC     INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

  Query Match           44.9%;  Score 623;  DB 2;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db     85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
          :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy     41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db    145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
          ||:||| |||:|||: ||:::  |: :||: :|  ||: :|||  |  |||: |  ::|
Qy    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
          : :|  | | :: : |:| | ||:|
Qy    161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   12
ID   US-08-471-057-14     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 14, Application US/08471057
XX
CC    Sequence 14, Application US/08471057
CC    Patent No. 6015687
CC     GENERAL INFORMATION:
CC       APPLICANT:  KIEFER, MICHAEL C.
```

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Db      61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db     121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
           ||:|:||||||||||||||||:||||||||||:|||||||||| | ||:|||||||
Qy     122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db     181 ALVTVGAFFASK 192
           ||||||||||||
Qy     181 ALVTVGAFFASK 192


RESULT    8
ID   US-08-798-897-6     STANDARD;     PRT;   192 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 6, Application US/08798897
XX
CC    Sequence 6, Application US/08798897
CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  192 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   192 AA; 20701 MW; 181510 CN;

  Query Match           95.7%;  Score 1326;  DB 1;  Length 192;
  Best Local Similarity  94.3%;  Pred. No. 2.75e-109;
  Matches   181;  Conservative    8;  Mismatches   2;  Indels   1;  Gaps   1;

Db       1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
           :||||:|||||| |||||:||||||||||||||||||||||||||||||||||||||||||
Qy       2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db      61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db     121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
           ||:|:||||||||||||||||:||||||||||:|||||||||| | ||:|||||||
Qy     122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db     181 ALVTVGAFFASK 192
           ||||||||||||
Qy     181 ALVTVGAFFASK 192


RESULT    9
ID   PCT-US95-04600-24     STANDARD;     PRT;   233 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 24, Application PC/TUS9504600
XX
CC    Sequence 24, Application PC/TUS9504600
CC     GENERAL INFORMATION:
CC       APPLICANT:  LA JOLLA CANCER RESEARCH FOUNDATION
CC       TITLE OF INVENTION:  Interaction of Proteins Involved in
CC       TITLE OF INVENTION:  a Cell Death Pathway
CC       NUMBER OF SEQUENCES:  29
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Campbell and Flores
CC         STREET:  4370 La Jolla Village Drive, Suite 700
CC         CITY:  San Diego
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  92122
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US95/04600
CC         FILING DATE:  12-APR-1995
CC         CLASSIFICATION:
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Imbra, Richard J.
CC         REGISTRATION NUMBER:  37,643
CC         REFERENCE/DOCKET NUMBER:  FP-LJ 1361
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (619) 535-9001
CC         TELEFAX:  (619) 535-8949
CC     INFORMATION FOR SEQ ID NO:  24:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  233 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
SQ   SEQUENCE   233 AA; 26063 MW; 275311 CN;

  Query Match           44.9%;  Score 623;  DB 4;  Length 233;
  Best Local Similarity  52.4%;  Pred. No. 7.82e-45;
  Matches    76;  Conservative   34;  Mismatches  32;  Indels   3;  Gaps   3;

Db      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
           :: ||:| |||||| |:||:||||::|||:|||:| | | || :|||: | ||||:||||
Qy      41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100

Db     145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
           ||:||| |||:|||: ||::: |: :||: :| ||: :||| | |||: | ::|
Qy     101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160

Db     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
           : :|  | | :: : |:| | ||:|
Qy     161 RLREG-N-WAVSTV-VTGAVALGAL 182


RESULT   10
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Db      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          :||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db    121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||||:|:||||||||||||||||:||||||||||:|||||||||| | ||:|||||||
Qy    122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    181 ALVTVGAFFASK 192
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RESULT 6
ID US-08-798-897-5 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 5, Application US/08798897
XX
CC Sequence 5, Application US/08798897
CC Patent No. 5789201
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 192 AA; 20689 MW; 183185 CN;

Query Match 96.1%; Score 1332; DB 1; Length 192;
Best Local Similarity 95.3%; Pred. No. 7.67e-110;
Matches 183; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

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Db      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          :||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61

Db     61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121

Db    121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
          ||||:|:||||||||||||||||:||||||||||:|||||||||| | ||:|||||||
Qy    122 VQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALG 180

Db    181 ALVTVGAFFASK 192
          ||||||||||||
Qy    181 ALVTVGAFFASK 192
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RESULT 7
ID US-08-978-523-6 STANDARD; PRT; 192 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08978523
XX
CC Sequence 6, Application US/08978523
CC Patent No. 5883229
CC GENERAL INFORMATION:
CC APPLICANT: Guastella, John
CC TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
CC TITLE OF INVENTION: Homologue
CC NUMBER OF SEQUENCES: 53
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC STREET: 1100 New York Avenue, N.W., Suite 600
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/978,523
CC FILING DATE: herewith
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/798,897
CC FILING DATE: February 11, 1997
CC CLASSIFICATION: 424
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Esmond, Robert W.
CC REGISTRATION NUMBER: 32,893
CC REFERENCE/DOCKET NUMBER: 1483.0140002
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-2600
CC TELEFAX: 202-371-2540
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 192 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 192 AA; 20701 MW; 181510 CN;

Query Match 95.7%; Score 1326; DB 2; Length 192;
Best Local Similarity 94.3%; Pred. No. 2.75e-109;
Matches 181; Conservative 8; Mismatches 2; Indels 1; Gaps 1;

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Db      1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
          :||||:|||||||| ||||||:||||||||||||||||||||||||||||||||||||||
Qy      2 PTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
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DE   Sequence 4, Application US/08978523
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CC    Sequence 4, Application US/08978523
CC    Patent No. 5883229
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/978,523
CC         FILING DATE:  herewith
CC         CLASSIFICATION:  424
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140002
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20832 MW; 183365 CN;

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Db     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Db    121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
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DE   Sequence 5, Application US/08978523
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CC    Patent No. 5883229
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/978,523
CC         FILING DATE:  herewith
CC         CLASSIFICATION:  424
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140002
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  5:
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CC         LENGTH:  192 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   192 AA; 20689 MW; 183185 CN;

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DE   Sequence 3, Application US/08978523
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CC    Sequence 3, Application US/08978523
CC    Patent No. 5883229
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/978,523
CC         FILING DATE:  herewith
CC         CLASSIFICATION:  424
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  424
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140002
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20820 MW; 185063 CN;
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  Query Match           96.9%;  Score 1343;  DB 2;  Length 193;
  Best Local Similarity  95.3%;  Pred. No. 7.37e-111;
  Matches   184;  Conservative    7;  Mismatches   1;  Indels   1;  Gaps   1;

Db      1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Qy    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179

Db    181 GALVTVGAFFASK 193
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DE   Sequence 4, Application US/08798897
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CC    Sequence 4, Application US/08798897
CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  4:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20832 MW; 183365 CN;

  Query Match           96.5%;  Score 1337;  DB 1;  Length 193;
  Best Local Similarity  94.3%;  Pred. No. 2.65e-110;
  Matches   182;  Conservative    8;  Mismatches   2;  Indels   1;  Gaps   1;
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MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 23 14:19:56 2000; MasPar time 5.42 Seconds
511.832 Million cell updates/sec

Tabular output not generated.

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Perfect Score: 1386
Sequence: 1 MPTPASTPDTRALVADFVGY.....VTGAVALGALVTVGAFFASK 192

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 30.635; Variance 141.077; scale 0.217

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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CC    Patent No. 5789201
CC     GENERAL INFORMATION:
CC       APPLICANT:  Guastella, John
CC       TITLE OF INVENTION:  Genes Coding For Bcl-y, a Bcl-2
CC       TITLE OF INVENTION:  Homologue
CC       NUMBER OF SEQUENCES:  53
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CC         STREET:  1100 New York Avenue, N.W., Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/798,897
CC         FILING DATE:  February 11, 1997
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Esmond, Robert W.
CC         REGISTRATION NUMBER:  32,893
CC         REFERENCE/DOCKET NUMBER:  1483.0140001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  202-371-2600
CC         TELEFAX:  202-371-2540
CC     INFORMATION FOR SEQ ID NO:  3:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  193 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   193 AA; 20820 MW; 185063 CN;
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